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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:31:17 ; Search time 217 Seconds
(without alignments)

5815.985 Million cell updates/sec

Title: US-09-493-601B-1

Perfect score: 710

Sequence: 1 atgtcgggcaataacatgtc.....tgacgtcactaagagccctt 710

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
- 7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/prodata/1/ina/backfileseq1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708.4	99.8	1486	2	US-09-022-940-4
2	708.4	99.8	1486	3	US-09-216-386-4
3	708.4	99.8	1556	3	US-09-629-645A-18
4	708.4	99.8	2417	3	US-09-629-645A-3
5	667.2	94.0	2421	3	US-09-949-016-4023
6	667.2	94.0	6421	3	US-09-949-016-15765
7	667.2	94.0	14126	3	US-09-949-016-15171
8	565	79.6	693	3	US-09-629-645A-10
9	556.4	78.4	727	3	US-09-629-645A-21
10	552.8	77.9	709	2	US-08-844-120-2
11	552.8	77.9	709	3	US-09-022-940-2
12	552.8	77.9	709	3	US-09-216-386-2
13	552.8	77.9	709	3	US-09-213-394-2
14	552.8	77.9	709	3	US-09-988-982-2
15	500	70.4	601	3	US-09-949-016-122098
16	500	70.4	601	3	US-09-949-016-142287
17	313.6	44.2	601	3	US-09-949-016-122099
18	313.6	44.2	601	3	US-09-949-016-142286
19	277.6	39.1	1624	3	US-09-013-881-15
20	277.6	39.1	1624	3	US-09-612-473-15
21	249.2	35.1	601	3	US-09-949-016-142288
22	212	29.9	457	3	US-09-621-976-2471
23	176.8	24.9	601	3	US-09-949-016-142289
24	172.4	24.3	559	3	US-09-612-473-49

25	156.8	22.1	601	3	US-09-949-016-142290
26	99.6	14.0	608	3	US-09-629-645A-20
27	75	10.6	675	3	US-09-540-236-1521
28	71.8	10.1	62909	3	US-09-596-002-32
29	69.2	9.7	975	3	US-09-216-001-2
30	69.2	9.7	975	3	US-08-878-862-2
31	68.2	9.6	852	3	US-09-599-360B-9
32	68.2	9.6	852	3	US-09-599-360B-61
33	68.2	9.6	852	3	US-09-513-999C-9
34	68.2	9.6	852	3	US-09-471-276-9
35	65.6	9.2	774	3	US-09-248-796A-1951
36	60.8	8.6	466	3	US-09-612-473-50
37	60.8	8.6	67181	3	US-09-949-016-13102
38	58.2	8.2	545	3	US-09-533-559-5020
39	53	7.5	260	3	US-09-612-473-48
40	45.6	6.4	777	3	US-09-252-991A-3689
41	41.4	5.8	278	3	US-09-313-294A-3545
42	41.2	5.8	255	3	US-09-248-796A-1952
43	40	5.6	260247	3	US-09-949-016-13358
44	39.4	5.5	601	3	US-09-949-016-112652
45	39.4	5.5	1732	3	US-09-023-655-741

ALIGNMENTS

RESULT 1

US-09-022-940-4
; Sequence 4, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,940
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1486 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-022-940-4

Query Match 99.8%; Score 708.4; DB 2; Length 1486;
Best Local Similarity 99.9%; Pred. No. 6.1e-234;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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US-09-629-645A-18
; Sequence 18, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 18
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (195)...(887)
US-09-629-645A-18

Query Match      99.8%; Score 708.4; DB 3; Length 1556;
Best Local Similarity 99.9%; Pred. No. 6.3e-234;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAACATGTCAACCCCGCTGCGCCGCATCGTCCCGCCGCGCCGGAAGGCC 60
DB 195 ATGTGCGGCAATAACATGTCAACCCCGCTGCGCCGCATCGTCCCGCCGCGCCGGAAGGCC 254

QY 61 ACCGCTGCGGTGATTTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGGCAGAAGCC 120
DB 255 ACCGCTGCGGTGATTTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGGCAGAAGCC 314

QY 121 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 180
DB 315 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 374

QY 181 GTTACATTAATAATGAACGTGCTATGCCCTCATGGTTTGATATTTGGGCTTTACACA 240
DB 375 GTTACATTAATAATGAACGTGCTATGCCCTCATGGTTTGATATTTGGGCTTTACACA 434

QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGACAGCAAAATATAAAGCTTTGATT 300
DB 435 GATTCACAGGAGATGAATCTGGGATTAACAGGACAGCAAAATATAAAGCTTTGATT 494

QY 301 GATCAAGAGTGAAGATGGCAATTCCTTCTAAGCAATTTATTTGGAGGGTTTCTCAG 360
DB 495 GATCAAGAGTGAAGATGGCAATTCCTTCTAAGCAATTTATTTGGAGGGTTTCTCAG 554

QY 361 GGAGGAGCTTTATCTTTTATATATCTGCCCTTACACACAGCAAACTGGCAGGTGTCAT 420
DB 555 GGAGGAGCTTTATCTTTTATATATCTGCCCTTACACACAGCAAACTGGCAGGTGTCAT 614

QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTGT 480
DB 615 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTGT 674

QY 481 AATAGAGATTTTCTATTTCTCAGTCCACGGGATTTGTGACCTTTGGTTCCCTTGATG 540
DB 675 AATAGAGATTTTCTATTTCTCAGTCCACGGGATTTGTGACCTTTGGTTCCCTTGATG 734

QY 541 TTTCGTTCTCTTACGGTGGAAAACTAAAAACAATTGGTGAATCCAGCCAAATGTGACCTTT 600
DB 735 TTTCGTTCTCTTACGGTGGAAAACTAAAAACAATTGGTGAATCCAGCCAAATGTGACCTTT 794

QY 601 AAAACCTATGAAGGTATGATGACAGTTGCTGTCAACAGCAAAATGATGATGTCAGCAA 660
DB 795 AAAACCTATGAAGGTATGATGACAGTTGCTGTCAACAGCAAAATGATGATGTCAGCAA 854

QY 661 TTTCATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTTAAGAGGCTTT 710
DB 855 TTTCATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTTAAGAGGCTTT 904
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US-09-629-645A-3
; Sequence 3, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 3
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(728)
US-09-629-645A-3

Query Match      99.8%; Score 708.4; DB 3; Length 2417;
Best Local Similarity 99.9%; Pred. No. 8.6e-234;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAACATGTCAACCCCGCTGCGCCGCATCGTCCCGCCGCGCCGGAAGGCC 60
DB 36 ATGTGCGGCAATAACATGTCAACCCCGCTGCGCCGCATCGTCCCGCCGCGCCGGAAGGCC 95

QY 61 ACCGCTGCGGTGATTTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGGCAGAAGCC 120
DB 96 ACCGCTGCGGTGATTTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGGCAGAAGCC 155

QY 121 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 180
DB 156 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 215

QY 181 GTTACATTAATAATGAACGTGCTATGCCCTCATGGTTTGATATTTGGGCTTTACACA 240
DB 216 GTTACATTAATAATGAACGTGCTATGCCCTCATGGTTTGATATTTGGGCTTTACACA 275

QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGACAGCAAAATATAAAGCTTTGATT 300
DB 276 GATTCACAGGAGATGAATCTGGGATTAACAGGACAGCAAAATATAAAGCTTTGATT 335

QY 301 GATCAAGAGTGAAGATGGCAATTCCTTCTAAGCAATTTATTTGGAGGGTTTCTCAG 360
DB 336 GATCAAGAGTGAAGATGGCAATTCCTTCTAAGCAATTTATTTGGAGGGTTTCTCAG 395

QY 361 GGAGGAGCTTTATCTTTTATATATCTGCCCTTACACACAGCAAACTGGCAGGTGTCAT 420
DB 396 GGAGGAGCTTTATCTTTTATATATCTGCCCTTACACACAGCAAACTGGCAGGTGTCAT 455

QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTGT 480
DB 456 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTGT 515

QY 481 AATAGAGATTTTCTATTTCTCAGTCCACGGGATTTGTGACCTTTGGTTCCCTTGATG 540
DB 516 AATAGAGATTTTCTATTTCTCAGTCCACGGGATTTGTGACCTTTGGTTCCCTTGATG 575

QY 541 TTTCGTTCTCTTACGGTGGAAAACTAAAAACAATTGGTGAATCCAGCCAAATGTGACCTTT 600
DB 576 TTTCGTTCTCTTACGGTGGAAAACTAAAAACAATTGGTGAATCCAGCCAAATGTGACCTTT 635

QY 601 AAAACCTATGAAGGTATGATGACAGTTGCTGTCAACAGCAAAATGATGATGTCAGCAA 660
DB 636 AAAACCTATGAAGGTATGATGACAGTTGCTGTCAACAGCAAAATGATGATGTCAGCAA 695

QY 661 TTTCATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTTAAGAGGCTTT 710
DB 696 TTTCATTGATAAACTCCTACCTCCAAATTTGATTGACGTCACTTAAGAGGCTTT 745
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RESULT 5
US-09-016-4023
; Sequence 4023, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4023
; LENGTH: 2421
; TYPE: DNA
; ORGANISM: Human
US-09-016-4023

Query Match 94.0%; Score 667.2; DB 3; Length 2421;
Best Local Similarity 97.9%; Pred. No. 1.6e-219;
Matches 697; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 ATGTGCGGCAATAACATGTCAACCCCGTGCCTGCGGCATCGTCCCGCCGCGCCGCGAAGGCC 60
Db 36 ATGTGCGGCAATAACATGTCAACCCCGTGCCTGCGGCATCGTCCCGCCGCGCCGCGAAGGCC 95

QY 61 ACCCGTGGCGGTGATTTCTGTCATGGATTGGAGATATCGGCGACGATGGGCGAGAAGCC 120
Db 96 ACCACTGAGGTGATTTCTGTCATGGATTGGAGATATCGGCGACGATGGGCGAGAAGCC 155

QY 121 TTGTCAGGTATCAGAGTTTCACATATCAATATATCTGCCGCATCGCCGATGTTAGGCT 180
Db 156 TTGTCAGGTATCAGAGTTTCACATATCAATATATCTGCCGCATCGCCGATGTTAGGCT 215

QY 181 GTT-ACATTAATATGAACGTGGCTATGCTTTCATGGTTTGATATATTTGGGCTTTTCCAC 239
Db 216 GTTAACATTAATATGAACGTGGCTATGCTTTCATGGTTTGATATATTTGGGCTTTTCCAC 275

QY 240 AGATTACAGGAGGTGATTCGGATTAAACAGGCGACAGAAAATATAAAGCTTTGAT 299
Db 276 AGATTACAGGAGGTGATTCGGATTAAACAGGCGACAGAAAATATAAAGCTTTGAT 335

QY 300 TGATCAAGAGTGAAGATGGCATTCCTTCTAACAGATTATTTGGGAGGGTTTCTCA 359
Db 336 TGATCAAGAGTGAAGATGGCATTCCTTCTAACAGATTATTTGGGAGGGTTTCTCA 395

QY 360 GGGAGAGCTTTATCTTTATATATCTGCTTACACAGCAGAAAATCGGAGGTGTAC 419
Db 396 GGGAGAGCTTTATCTTTATATATCTGCTTACACAGCAGAAAATCGGAGGTGTAC 455

QY 420 TGCACGTCTGCTGGCTTCCACTTTGGGCTTCCCTTCCACAGGCTTATCGGTGGTGC 479
Db 456 TGCACGTCTGCTGGCTTCCACTTTGGGCTTCCCTTCCACAGGCTTATCGGTGGTGC 515

QY 480 TAATAGAGATATTTCTATCTCCAGTGCACGGGATTTGTGACCTTTGGTTCCCTGTAT 539
Db 516 TAATAGAGATATTTCTATCTCCAGTGCACGGGATTTGTGACCTTTGGTTCCCTGTAT 575

QY 540 GTTTGGTCTCTTACGGTGGAAAACT-AAAAAATTTGGTGAATCCAGCAATGTGACCT 598
Db 576 GTTTGGTCTCTTACGGTGGAAAACTAAAAAATTTGGTGAATCCAGCAATGTGACCT 635

QY 599 TTAACAACCTATGAGGTATGATGCAAGTTCTGTGCAACAGGAAATGATGGATGTCAGC 658
Db 636 TTAACAACCTATGAGGTATGATGCAAGTTCTGTGCAACAGGAAATGATGGATGTCAGC 695

QY 659 AATTCATTGATAAACTCTACCTCCAATTGATTGACGTCACTAAGAGCCTT 710
Db 696 AATTCATTGATAAACTCTACCTCCAATTGATTGACGTCACTAAGAGCCTT 747

RESULT 6
US-09-949-016-15765
; Sequence 15765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15765
; LENGTH: 6421
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15765

Query Match 94.0%; Score 667.2; DB 3; Length 6421;
Best Local Similarity 97.9%; Pred. No. 3.1e-219;
Matches 697; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 ATGTGCGGCAATAACATGTCAACCCCGTGCCTGCGGCATCGTCCCGCCGCGCCGCGAAGGCC 60
Db 2036 ATGTGCGGCAATAACATGTCAACCCCGTGCCTGCGGCATCGTCCCGCCGCGCCGCGAAGGCC 2095

QY 61 ACCCGTGGCGGTGATTTCTGTCATGGATTGGAGATATCGGCGACGATGGGCGAGAAGCC 120
Db 2096 ACCACTGAGGTGATTTCTGTCATGGATTGGAGATATCGGCGACGATGGGCGAGAAGCC 2155

QY 121 TTGTCAGGTATCAGAGTTTCACATATCAATATATCTGCCGCATCGCCGATGTTAGGCT 180
Db 2156 TTGTCAGGTATCAGAGTTTCACATATCAATATATCTGCCGCATCGCCGATGTTAGGCT 2215

QY 181 GTT-ACATTAATATGAACGTGGCTATGCTTTCATGGTTTGATATATTTGGGCTTTTCCAC 239
Db 2216 GTTAACATTAATATGAACGTGGCTATGCTTTCATGGTTTGATATATTTGGGCTTTTCCAC 2275

QY 240 AGATTACAGGAGGTGATTCGGATTAAACAGGCGACAGAAAATATAAAGCTTTGAT 299
Db 2276 AGATTACAGGAGGTGATTCGGATTAAACAGGCGACAGAAAATATAAAGCTTTGAT 2335

QY 300 TGATCAAGAGTGAAGATGGCATTCCTTCTAACAGATTATTTGGGAGGGTTTCTCA 359
Db 2336 TGATCAAGAGTGAAGATGGCATTCCTTCTAACAGATTATTTGGGAGGGTTTCTCA 2395

QY 360 GGGAGAGCTTTATCTTTATATATCTGCTTACACAGCAGAAAATCGGAGGTGTAC 419
Db 2396 GGGAGAGCTTTATCTTTATATATCTGCTTACACAGCAGAAAATCGGAGGTGTAC 2455

QY 420 TGCACGTCTGCTGGCTTCCACTTTGGGCTTCCCTTCCACAGGCTTATCGGTGGTGC 479
Db 2456 TGCACGTCTGCTGGCTTCCACTTTGGGCTTCCCTTCCACAGGCTTATCGGTGGTGC 2515

QY 480 TAATAGAGATATTTCTATCTCCAGTGCACGGGATTTGTGACCTTTGGTTCCCTGTAT 539
Db 2516 TAATAGAGATATTTCTATCTCCAGTGCACGGGATTTGTGACCTTTGGTTCCCTGTAT 2575

QY 540 GTTTGGTCTCTTACGGTGGAAAACT-AAAAAATTTGGTGAATCCAGCAATGTGACCT 598
Db 540 GTTTGGTCTCTTACGGTGGAAAACT-AAAAAATTTGGTGAATCCAGCAATGTGACCT 598

2576	GTTTGGTTCCTTACGGTTGAA	AACTAA	AAAA	CATTGGTGAATCCAGCAATGTGACCT	2635
Db					
599	TTAAAACTATGAAGGTATGATGACACATTCGTT	CGTGTCAACAGGA	AAATGATGGATGTC	CAAGC	658
Qy					
2636	TTAAAACTATGAAGGTATGATGACACATTCGTT	CGTGTCAACAGGA	AAATGATGGATGTC	CAAGC	2695
Db					
659	AAATTCATTGTATAAACTCCTACCTCCAATTG	ATTGATCGTCACTAAGAGG	CCTT		710
Qy					
2696	AAATTCATTGTATAAACTCCTACCTCCAATTG	ATTGATCGTCACTAAGAGG	CCTT		2747
Db					

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RESULT 7
US-09-949-016-15171/c
; Sequence 15171, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15171
; LENGTH: 14126
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15171

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Query Match	94.08;	Score 667.2;	DB 3;	Length 14126;
Best Local Similarity	97.99;	Pred. No. 5.3e-219;		
Matches 697;	Conservative 0;	Mismatches 13;	Indels 2;	Gaps 2;
Qy	1	ATGTGGCGCAATACATGTCAACCCCGCTGCCCGCCATCGTGC	CGCGCGCGCCGGAAGGCC	60
Db	2735	ATGTGGCGCAATACATGTCAACCCCGCTGCCCGCCATCGTGC	CGCGCGCGCCGGAAGGCC	2676
Qy	61	ACCGCTCGCGTGATTTTCTCGATGGATTGGGAGATAC	TGGGACCGGATGGGAGAGCC	120
Db	2675	ACCACTGAGGTGATTTTCTCGATGGATTGGGAGATAC	TGGGACCGGATGGGAGAGCC	2616
Qy	121	TTTGCAGGTATCAGAAGTTACATATCAAAATATATCTGCCCGCATGGCCCTGTGGCCCT	180	
Db	2615	TTTGCAGGTATCAGAAGTTACATATCAAAATATATCTGCCCGCATGGCCCTGTGGCCCT	2556	
Qy	181	GTTT-ACATTTAAATATGAACGTGGGTATGCCTTCATGGTTTGATATATTGGGCTTTTCACC	239	
Db	2555	GTTTAAACATTTAAATATGAACATGAGTATGCCTTCATGGTTTGATATATTGGGCTTTTCACC	2496	
Qy	240	AGATTTCACAGGAGATGAATCTGGGATTTAAACAGGACGACGAAATATAAAAGCTTTTGAT	299	
Db	2495	AGATTTCACAGGAGATGAATCTGGGATTTAAACAGGACGACGAAATATAAAAGCTTTTGAT	2436	
Qy	300	TGATCAAGAAGTGAAGAATGGCATTCCTTTCAACAGAAATTTATTTTGGGAGGGTTTTCTCA	359	
Db	2435	TGATCAAGAAGTGAAGAATGGCATTCCTTTCTTAAACAGAAATTTATTTTGGGAGGGTTTTCTCA	2376	
Qy	360	GGGAGGAGCTTTATCTTTTATATATCTGGCTTACCACACGACAGAAACTGGCAGGTGTCAC	419	
Db	2375	GGGAGGAGCTTTATCTTTTATATATCTGGCTTACCACGACAGAAACTGGCAGGTGTCAC	2316	
Qy	420	TGCACCTCAGTTGCTGGCTTCCACATTCGGGGCTTCCCTTCCACACAGGGTCCTATCCGCTGGTGC	479	
Db	2315	TGCACCTCAATTCGCTGGCTTCCACATTCGGGGCTTCCCTTCCACACAGGGTCCTATCCGCTGGTGC	2256	
Qy	480	TAATAGAGATATTTCTATTTCTCCAGTGCCACGGGATTTGTGACCCCTTTGGTCCCCCTTGAT	539	

Qy	Db	Sequence	Qy	Db	Sequence
598	2255	TAATACAGATATTTCTATTCTCCAGTGCCACGGGATTTGTACCCCTTGTGTTCCCTGAT	2074	2075	AAATTCATTGATAAATCTTACCTCCAAATTGATTGAGCTCACTAAGAGGCCCT
599	540	GTTTGGTTCCTTACGGTGGAAAACT-AAAAACATTGGTGAATCCAGCCAAATGTGACCT	2075	659	AATTCATTGATAAATCTTACCTCCAAATTGATTGAGCTCACTAAGAGGCCCT
2136	2195	GTTTGGTTCCTTACGGTGGAAAACTTAAAAACATTGGTGAATCCAGCCAAATGTGACCT	2076	2135	TTAAAAACCTATGAAGGTATGATGCACAGTTCTGTTGTCACACAGGAAATGATGGATGTCAAAC
658	599	TTAAAAACCTATGAAGGTATGATGCACAGTTCTGTTGTCACACAGGAAATGATGGATGTCAAAC	2077	2196	TAATACAGATATTTCTATTCTCCAGTGCCACGGGATTTGTACCCCTTGTGTTCCCTGAT
710	2135	TTAAAAACCTATGAAGGTATGATGCACAGTTCTGTTGTCACACAGGAAATGATGGATGTCAAAC	2078	659	AATTCATTGATAAATCTTACCTCCAAATTGATTGAGCTCACTAAGAGGCCCT
2024	659	AATTCATTGATAAATCTTACCTCCAAATTGATTGAGCTCACTAAGAGGCCCT	2025	2075	AAATTCATTGATAAATCTTACCTCCAAATTGATTGAGCTCACTAAGAGGCCCT

RESULT 8
 US-09-629-645A-10
 Sequence 10, Application US/09629645A
 Patent No. 6365354
 GENERAL INFORMATION:
 APPLICANT: C. Frank Bennett
 APPLICANT: Jacqueline Wyatt
 TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
 FILE REFERENCE: RTS-0137
 CURRENT APPLICATION NUMBER: US/09/629,645A
 CURRENT FILING DATE: 2000-07-31
 NUMBER OF SEQ ID NOS: 164
 SEQ ID NO 10
 LENGTH: 693
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(693)
 US-09-629-645A-10

Query Match	79.6%;	Score 565;	DB 3;	Length 693;
Best Local Similarity	88.5%;	Pred. No. 1.5e-184;		
Matches 613;	Conservative 0;	Mismatches 80;	Indels 0;	Gaps 0;
Qy	1	ATGTGGCGCAATACATGTCAACCCCGCTGCCCGCCCATCTGTGCCGCGCCCGCGAAGGCC	60	
Db	1	ATGTGGCGCAACACATGTCCGCTCGCATGCCCGCGTGTGTGCCGCGCCCGCGAAGGCC	60	
Qy	61	ACCGCTCGCGTGTATTTTCTTGCACTGATTTGGAGATATCTGGCACGCGATGGCGAAGGCC	120	
Db	61	ACCGCCCGGTTATTTTCTTTCAGGATTTGGAGATACAGGGCATGATGGCGAAGGCC	120	
Qy	121	TTTTCAGGATATCAGAAGTTCACATATCAAAATATATCTGCCCGCATGCCCTGTGTAGCGCT	180	
Db	121	TTTTCAGGATCAAAAGTCCCAATCAATACATCTGCCATGCCCCCTGTGATGCCA	180	
Qy	181	GTTCATATTAATATGAACGTGGGTATGCCCTTCATGGTTTGATATATTGGCTTTTCACCA	240	
Db	181	GTCACTTAAATATGAATATGGCTTATGCCCTTCTTGGTTTGATATCGTTGGACTTTTCACCA	240	
Qy	241	GATTCACAGGAGTGAATCTGGGATTAACACGCGACGAGAAATATAAAGCTTTTCATT	300	
Db	241	GATTCCAGGAGTGAATCTGGAAATTAACACGCGACGAGAAACCGTTAAAGCCTTGATA	300	
Qy	301	GATCAAGAAGTGAAGAATGGCATTCCTTTCTAAACAGAAATATATTTGGGAGGGTTTTCTCAG	360	
Db	301	GATCAAGAAGTGAAGAATGGCATTCCTTCTTAAACAGGATATATTTGGGAGGATTTTCTCAG	360	
Qy	361	GGAGGAGCTTTATCTTTTATATCTATGCCCTTTACCAACACAGCAGAAACTGGCAGGTGTCACT	420	
Db	361	GGAGGCGCTTGTCTTTTATACATCTGTCTCACACACAGCAGAAACTGGCTGGTGTCACT	420	
Qy	421	GCACTCAGTTGCTGGCTTCCACTTGGGGCTTCCCTTCCACAGGCTCTCTATCGGTTGGTCT	480	
Db	421	GCACTCAGTTGCTGGCTTCCACTTGGGGCTTCTGTTTTTTCACAGGGGCGCATCAACAGTGTCT	480	

Db 669 TTCATTGATAAACTCCTACTCTCAATTCATTGACGTCACTA 709

RESULT 12

US-09-216-386-2
; Sequence 2, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-216-386-2

Query Match 77.9%; Score 552.8; DB 3; Length 709;
Best Local Similarity 89.9%; Pred. No. 2.5e-180;
Matches 630; Conservative 1; Mismatches 4; Indels 66; Gaps 1;

QY 1 ATGTGGGCAATAACATGTCACCCCGCTGCCCGCATGTCGCCCGCCGCGGAGGCC 60
DB 75 ATGTGGGCAATAACATGTCACCCCGCTGCCCGCATGTCGCCCGCCGCGGAGGCC 134
QY 61 ACCGCTGCGGTGATTTCTCTGATGATGGGAGATCTGGGCACGGATGGGACAGGCC 120
DB 135 ACCGCTGCGGTGATTTCTCTGATGATGGGAGATCTGGG----- 175
QY 121 TTTCAGGTATCAGAAGTTTACATATCAATATATCTGCCCGCATGCGCTTTAGGCT 180
DB 176 -----GCCTGTAGGCT 188
QY 181 GTTACATTAAATATGAACGTGCTATGCCCTTCATGTTGATATATTGGGCTTTACCA 240
DB 189 GTTACATTAAATATGAACGTGCTATGCCCTTCATGTTGATATATTGGGCTTTACCA 248
QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGACGACAGAAAATATAAAGCTTTGAT 300
DB 249 GATTCACAGGAGATGAATCTGGGATTAACAGGACGACAGAAAATATAAAGCTTTGAT 308
QY 301 GATCAAGAGTGAAGATGGCAATTCCTTCTAAACAGAAATTTTGGAGGGTTTCTCAG 360
DB 309 GATCAAGAGTGAAGATGGCAATTCCTTCTAAACAGAAATTTTGGAGGGTTTCTCAG 368

QY 361 GGAGGAGCTTTATCTTTATATACCTTACCAACAGCAGAAACTGCGAGGTGTCCT 420
DB 369 GGAGGAGCTTTATCTTTATATACCTTACCAACAGCAGAAACTGCGAGGTGTCCT 428
QY 421 GCACCTAGTGTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTGT 480
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QY 541 TTTGGTTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAGCCCAATGACCTTT 600
DB 549 TTTGGTTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAGCCCAATGACCTTT 608
QY 601 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGATCAAGCAA 660
DB 609 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGATGATCAAGCAA 668
QY 661 TTCATTGATAAACTCCTACTCTCAATTCATTGACGTCACTA 701
DB 669 TTCATTGATAAACTCCTACTCTCAATTCATTGACGTCACTA 709

RESULT 13

US-09-213-394-2
; Sequence 2, Application US/09213394
; Patent No. 6319701
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,394
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT19
; CLONE: 2676650
; US-09-213-394-2

Query Match 77.9%; Score 552.8; DB 3; Length 709;

Best Local Similarity 89.9%; Pred. No. 2.5e-180;
Matches 630; Conservative 1; Mismatches 4; Indels 66; Gaps 1;
QY 1 ATGTGGGCAATTAACATGTCACCCCGCTGCCCGCATCGTGGCCGCCCGCGGAGGCC 60
DB 75 ATGTGGGCAATTAACATGTCACCCCGCTGCCCGCATCGTGGCCGCCCGCGGAGGCC 134
QY 61 ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGACGCGATGGGAGAACGC 120
DB 135 ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGAGAACGC 175
QY 121 TTTCAGGTATCAGAAGTTCACATATCAATATATCTGCCCGCATCGCTGTAGGCCT 180
DB 176 -----GCTGTAGGCCT 188
QY 181 GTTACATTAAATATGAACGTGGCTATGCCCTTCATGGTTGATATTTGGGCTTTTCCACCA 240
DB 189 GTTACATTAAATATGAACGTGGCTATGCCCTTCATGGTTGATATTTGGGCTTTTCCACCA 248
QY 241 GATTACAGGAGGATGAATCTGGGATTTAAACAGGACGACAGAAATATAAAGCTTTGATT 300
DB 249 GATTACAGGAGGATGAATCTGGGATTTAAACAGGACGACAGAAATATAAAGCTTTGATT 308
QY 301 GATCAAGAGTGAAGATGGCATTCCTTCTAACAGAAATATTTTGGGAGGTTTCTCAG 360
DB 309 GATCAAGAGTGAAGATGGCATTCCTTCTAACAGAAATATTTTGGGAGGTTTCTCAG 368
QY 361 GGAGGAGCTTATCTTTATATCTGCTTACCACAGCAGAGAACTGGCAGGTGTCACT 420
DB 369 GGAGGAGCTTATCTTTATATCTGCTTACCACAGCAGAGAACTGGCAGGTGTCACT 428
QY 421 GCACTCAGTGTGCTTCCACTTTCAGTTCCTTCCACAGGCTCTATCGGTGGTGTCT 480
DB 429 GCACTCAGTGTGCTTCCACTTTCAGTTCCTTCCACAGGCTCTATCGGTGGTGTCT 488
QY 481 AATAGAGATTTCTATTTCTCAGTGCACGGGATTTGACCCCTTTTGGTTCCTCGATG 540
DB 489 AATAGAGATTTCTATTTCTCAGTGCACGGGATTTGACCCCTTTTGGTTCCTCGATG 548
QY 541 TTTGGTCTCTACGGTGGAAAACTAAACAACTTGGTGAATCCAGCAATGTGACCTTT 600
DB 549 TTTGGTCTCTACGGTGGAAAACTAAACAACTTGGTGAATCCAGCAATGTGACCTTT 608
QY 601 AAAACCTATGAAGTATGATGCAAGTTCGTGTCAACAGAGAAATGATGATGTCAAGCAA 660
DB 609 AAAACCTATGAAGTATGATGCAAGTTCGTGTCAACAGAGAAATGATGATGTCAAGCAA 668

RESULT 14

US-09-988-982-2
; Sequence 2, Application US/09988982
; Patent No. 6838245
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Shah, Purvi
; Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

SOFTWARE: PastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/988,982
FILING DATE: 19-No. 6838245-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT19
CLONE: 2676650
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-988-982-2
Query Match 77.9%; Score 552.8; DB 3; Length 709;
Best Local Similarity 89.9%; Pred. No. 2.5e-180;
Matches 630; Conservative 1; Mismatches 4; Indels 66; Gaps 1;
QY 1 ATGTGGGCAATTAACATGTCACCCCGCTGCCCGCATCGTGGCCGCCCGCGGAGGCC 60
DB 75 ATGTGGGCAATTAACATGTCACCCCGCTGCCCGCATCGTGGCCGCCCGCGGAGGCC 134
QY 61 ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGACGCGATGGGAGAACGC 120
DB 135 ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGAGAACGC 175
QY 121 TTTCAGGTATCAGAAGTTCACATATCAATATATCTGCCCGCATCGCTGTAGGCCT 180
DB 176 -----GCTGTAGGCCT 188
QY 181 GTTACATTAAATATGAACGTGGCTATGCCCTTCATGGTTGATATTTGGGCTTTTCCACCA 240
DB 189 GTTACATTAAATATGAACGTGGCTATGCCCTTCATGGTTGATATTTGGGCTTTTCCACCA 248
QY 241 GATTACAGGAGGATGAATCTGGGATTTAAACAGGACGACAGAAATATAAAGCTTTGATT 300
DB 249 GATTACAGGAGGATGAATCTGGGATTTAAACAGGACGACAGAAATATAAAGCTTTGATT 308
QY 301 GATCAAGAGTGAAGATGGCATTCCTTCTAACAGAAATATTTTGGGAGGTTTCTCAG 360
DB 309 GATCAAGAGTGAAGATGGCATTCCTTCTAACAGAAATATTTTGGGAGGTTTCTCAG 368
QY 361 GGAGGAGCTTATCTTTATATCTGCTTACCACAGCAGAGAACTGGCAGGTGTCACT 420
DB 369 GGAGGAGCTTATCTTTATATCTGCTTACCACAGCAGAGAACTGGCAGGTGTCACT 428
QY 421 GCACTCAGTGTGCTTCCACTTTCAGTTCCTTCCACAGGCTCTATCGGTGGTGTCT 480
DB 429 GCACTCAGTGTGCTTCCACTTTCAGTTCCTTCCACAGGCTCTATCGGTGGTGTCT 488
QY 481 AATAGAGATTTCTATTTCTCAGTGCACGGGATTTGACCCCTTTTGGTTCCTCGATG 540
DB 489 AATAGAGATTTCTATTTCTCAGTGCACGGGATTTGACCCCTTTTGGTTCCTCGATG 548
QY 541 TTTGGTCTCTACGGTGGAAAACTAAACAACTTGGTGAATCCAGCAATGTGACCTTT 600
DB 549 TTTGGTCTCTACGGTGGAAAACTAAACAACTTGGTGAATCCAGCAATGTGACCTTT 608
QY 601 AAAACCTATGAAGTATGATGCAAGTTCGTGTCAACAGAGAAATGATGATGTCAAGCAA 660
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RESULT 15
US-09-949-016-122098
; Sequence 122098, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122098
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-122098

Query Match 70.4%; Score 500; DB 3; Length 601;
Best Local Similarity 97.5%; Pred. No. 4.2e-162;
Matches 517; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

QY 182 TTACATTAATAATGAACGTGGCTATGCCCTTCATGGTTTGATATATTGGGCTTTCAACCAG 241
Db 3 TAACATTAATAATGAACATAGCTATGCCCTTCATGGTTTGATATATTGGGCTTTCAACCAG 62

QY 242 ATTCACAGGAGGATGAATCTGGGATTAAACAGGCAGCAGAAAATATAAAAGCTTTGATTG 301
Db 63 ATTCACAGGAGGATGAATCTGGGATTAAACAGGCAGCAGAAAATATAAAAGCTTTGATTG 122

QY 302 ATCAGAAGTGAAGATGGCATTCCTCTAACAGAAATATTTGGAGGGTTTCTCAGG 361
Db 123 ATCAGAAGTGAAGATGGCATTCCTCTAACAGAAATATTTGGAGGGTTTCTCAGG 182

QY 362 GAGGAGCTTTATCTTTATATATCTGCCCTTACCACACAGCAGAAACTGGCAGGTGTCACGTG 421
Db 183 GAGGAGCTTTATCTTTATATATCTGCCCTTACCACAGCAGAAACTGGCAGGTGTCACGTG 242

QY 422 CACTCAGTTGCTGGCTTCACATTCGGGGCTTCCCTCCACAGGGTCCCTATCGGTGGTGCTA 481
Db 243 CACTCAATTTGCTGGCTTCCACATTTGGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTGCTA 302

QY 482 ATAGAGATATTTCTATTTCTCCAGTCCAGGGGATTTGACCCCTTTGGTTCCCTGATGT 541
Db 303 ATAGAGATATTTCTATTTCTCCAGTCCAGGGGATTTGACCCCTTTGGTTCCCTGATGT 362

QY 542 TTGGTTCTCTTACGGTGGAAAACT-AAAAACATTTGGTGAATCCAGCCCAATGTGACCTTT 600
Db 363 TTGGTTCTCTTACGGTGGAAAACTAAAAACATTTGGTGAATCCAGCCCAATGTGACCTTT 422

QY 601 AAAACCTATGAAGGTATGATGCACAGTTGCTGTCAAAGAAATGATGGATGTCAAGCAA 660
Db 423 AAAACCTATGAAGGTATGATGCACAGTTGCTGTCAAAGAAATGATGGATGTCAAGCAA 482

QY 661 TTCAATTGATAAACTCCTACCTCCAATTGATTGACGTCACTA 710
Db 483 TTCAATTGATAAACTCCTACCTCCAATTGATTGACGTCACTA 532
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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2: gb_in.*
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6: gb_pat.*
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8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Database :				GenEmbl.*			
1: gb_ba.*				1: gb_ba.*			
2: gb_in.*				2: gb_in.*			
3: gb_env.*				3: gb_env.*			
4: gb_om.*				4: gb_om.*			
5: gb_ov.*				5: gb_ov.*			
6: gb_pat.*				6: gb_pat.*			
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RESULT 1

AF291053

LOCUS

Homo sapiens acyl-protein thioesterase-1 mRNA

PRI 20-NOV-2000

linear

complete cds.

760 bp

AF291053

AF291053

AF291053.1

GI:9965371

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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AX780162

Sequence

U97147

Oryctolagus

U97146

Rattus norv

BC085750

Rattus no

D63885

Rat liver m

BC013536

Mus muscu

BC052848

Mus muscu

BD134996

Human nuc

AR018183

Sequence

AR203091

Sequence

U89352

Mus muscu

U97148

Oryctolagus

CT010201

Mus muscu

AR203102

Sequence

AR028701

Sequence

AR079196

Sequence

AR104346

Sequence

AR178569

Sequence

BD191689

Human lys

AR629275

Sequence.

AC127599

Rattus no

AC116241

Rattus no

AC11839

Rattus no

AC118121

Rattus no

AC099137

Rattus no

AC073054

Homo sapi

AB168430

Macaca fa

AF291053

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 760)

Devedjiev,Y., Dauter,Z., Kuznetsov,S.R., Jones,T.L. and Derwenda,Z.S.

Crystal structure of the human acyl protein thioesterase I from a single X-ray data set to 1.5 A

Structure Fold. Des. 8 (11), 1137-1146 (2000)

11080636

2 (bases 1 to 760)

Kuznetsov,S.R. and Jones,T.L.Z.

Direct Submission

Submitted (28-JUL-2000) Metabolic Disease Branch, National Institute of Diabetes and Digestive and Kidney Diseases, 9000 Rockville Pike, Bldg.10, Room 9C112, Bethesda, MD 20892, USA

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

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/notes="hydrolase; APT-1"

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/evidence=not experimental

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
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2	708.4	99.8	1348 6 AX780008 Sequence
3	708.4	99.8	1381 8 BC010397 Homo sapi
4	708.4	99.8	1441 8 BC008652 Homo sapi
5	708.4	99.8	1486 6 AR079197 Sequence
6	708.4	99.8	1486 6 AR104347 Sequence
7	708.4	99.8	1486 6 BD191690 Human lys
8	708.4	99.8	1556 6 AR203099 Sequence
9	708.4	99.8	1556 8 AF052112 Homo sapi
10	708.4	99.8	2417 6 CQ894709 Sequence
11	708.4	99.8	2417 6 CQ896205 Sequence
12	708.4	99.8	2417 6 AR203084 Sequence
13	708.4	99.8	2417 6 AX256070 Sequence
14	708.4	99.8	2417 6 AF081281 Homo sapi
15	708.4	99.8	2600 6 CQ493329 Sequence
16	689.8	97.2	693 8 CR457103 Homo sapi
17	662.4	93.3	49616 8 AL365267 Human DNA
18	614	86.5	154252 8 AC004062 Homo sapi

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34
/note="alternate site of translation initiation"
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Query Match 99.8%; Score 708.4; DB 8; Length 760;
Best Local Similarity 99.9%; Pred. No. 1.4e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGCGGCAATAACATGTCACCCGCTGCCCGCATCGTGCCGCGCCGCGGAAGGCC 60
DB 19 ATGTGCGGCAATAACATGTCACCCGCTGCCCGCATCGTGCCGCGCCGCGGAAGGCC 78
QY 61 ACCGCTGCGGTGATTTCTCGATGATGGAGATCTGGGACGCGATGGGCGAGAAGCC 120
DB 79 ACCGCTGCGGTGATTTCTCGATGATGGAGATCTGGGACGCGATGGGCGAGAAGCC 138
QY 121 TTTCAGGTATCAGAAAGTTCAATATCAATATATCTGCCCGCATGGCTGTAGGCCT 180
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QY 481 AATAGAGATTTCTATTCTTCCAGTGCCACGGGATTTGACCCCTTTGGTTCCTCCTGATG 540
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LOCUS
Sequence 2165 from Patent WO03039443.
AX780008
AX780008.1 GI:32697002
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1
AUTHORS
Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,
Dugas, M., Bils, R., Brors, B. and Mergenthaler, S.

Novel genetic markers for leukemias
Patent: WO 03039443-A 2165 15-MAY-2003;
Deutsches Krebsforschungszentrum (DKFZ);
Ludwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torsten,
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)
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/mol_type="unassigned DNA"
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Query Match 99.8%; Score 708.4; DB 6; Length 1348;
Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGCGGCAATAACATGTCACCCGCTGCCCGCATCGTGCCGCGCCGCGGAAGGCC 60
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QY 61 ACCGCTGCGGTGATTTCTCGATGATGGAGATCTGGGACGCGATGGGCGAGAAGCC 120
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RESULT 3
BC010397
LOCUS
DEFINITION
Homo sapiens lysophospholipase I, mRNA (cDNA clone MGC:13688
IMAGE:4109335), complete cds.
ACCESSION
BC010397
VERSION
BC010397.1 GI:14714525
KEYWORDS
MGC.

SOURCE ORGANISM	Homo sapiens (human)
REFERENCE AUTHORS	Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Donald, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL PUBLISHED	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
REFERENCE AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (09-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabs-x@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: CLONTECH Laboratories, Inc. DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) http://www.systemsbio.org Contact: amadansystemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
FEATURES source	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: f Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20302148. Location/Qualifiers 1. .1381 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:13688 IMAGE:4109335" /tissue_type="Bone marrow, acute myelogenous leukemia" /clone_lib="NIH_MGC_55" /lab_host="DH10B" /note="Vector: pDNR-LIB" 1. .1381 /gene="LYPLAI" /note="synonyms: LPL1, APT-1, LYSOPLA" /db_xref="GeneID:10434" /db_xref="MIM:605599"
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ORIGIN	Query Match 99.8%; Score 708.4; DB 8; Length 1381; Best Local Similarity 99.9%; Pred. No. 1.5e-190; Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB	7 ATGTGGGCAATAAATGATGTCACACCGCGCTGCGCGCATCGTCCCGCCCGCGGAGGCC 66
QY	61 ACCGCTGCGGTGATTTCTTCGATGGATTGGGAGATCTTGGGACGCGATGGGAGAGCC 120
DB	67 ACCGCTGCGGTGATTTCTTCGATGGATTGGGAGATCTTGGGACGCGATGGGAGAGCC 126
QY	121 TTTGAGGTATCAGAGTTTCATATCAATATATCTGCCCGCATCGGCTGTAGGCTT 180
DB	127 TTTGAGGTATCAGAGTTTCATATCAATATATCTGCCCGCATCGGCTGTAGGCTT 186
QY	181 GTTACATTAATAATGAACTGCTGCTTCCCTTTCATGTTTGTATATTTGGGCTTTCACCA 240
DB	187 GTTACATTAATAATGAACTGCTGCTTCCCTTTCATGTTTGTATATTTGGGCTTTCACCA 246
QY	241 GATTCACAGGAGTGAATCTGGGATTAAACAGGACGAGAAATATAAAGCTTTGATT 300
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QY	301 GATCAAGAGTGAAGAAATGGCAATTCCTTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 360
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QY	361 GGAGAGCTTTTATCTTTTATATCTGCTTACACACAGCAGAAATCGGAGGTGTCACCT 420
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DB	427 GCACCTCAGTGTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTCT 486
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DB	487 AATAGAGATATTTCTTATCTCCAGTGCACGGGGATTGTACCCCTTTGGTTCCTCCGTATG 546
QY	541 TTTGGTTCTTACCGTGGAAAACTTAAAAACATTGGTGAATCCAGCAATGTGACCTTT 600
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DB	607 AAAACCTATGAGGTATGATGACAGTTCGTGTCACAGGAAATGATGGATGTCAAGCAA 666
QY	661 TTCATTGATAAACTCCCTACCTCCAAATTGATTGACGTCACTAAGAGGCTT 710
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RESULT 4
BC008652
LOCUS
DEFINITION
Homo sapiens lysophospholipase I, mRNA (cDNA clone MGC:9121
IMAGE:3865775), complete cds.
ACCESSION
BC008652
VERSION
BC008652.2
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
BC008652 1441 bp mRNA linear PRI 30-JUN-2004
IMAGE:3865775, complete cds.
BC008652
BC008652.2 GI:34194083
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE AUTHORS

1 (bases 1 to 1441)
Strausberg R.L., Fellings, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wegner, L., Shemen, C.M., Schuler, G.D., Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wille, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kerteman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1441)
Strausberg, R.
Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

TITLE

JOURNAL PUBLISHED REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 25, 2003 this sequence version replaced gi:14250433.
Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 13 Row: e Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20302148.

FEATURES source

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AR079197
LOCUS
DEFINITION
ACCESSION
VERSION
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AR079197.1 GI:10005943
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Unknown.
Unclassified.

RESULT 5

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LOCUS
DEFINITION
ACCESSION
VERSION
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AR079197.1 GI:10005943
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Unclassified.

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ORIGIN

Query Match 99.8%; Score 708.4; DB 8; Length 1441;
Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGCGGCAATAAATGTCACACCGCGTCCCGCATCGTCCCGCGCCCGGAGGCC 60
DB 83 ATGTGCGGCAATAAATGTCACACCGCGTCCCGCATCGTCCCGCGCCCGGAGGCC 142
QY 61 ACCGCTGCGGTGATTTCTCTGTCAGTGGAGATCTGGGCACCGGATGGCAGAGCC 120
DB 143 ACCGCTGCGGTGATTTCTCTGTCAGTGGAGATCTGGGCACCGGATGGCAGAGCC 202
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REFERENCE 1 (bases 1 to 1486)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lysophospholipase
JOURNAL Patent: US 5965423-A 4 12-OCT-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 616 TTTGGTTCTTACGGTGGAAAACCTAAACAACTTGGTGAATCCAGCCATGTGACCTTT 675

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DEFINITION Sequence 4 from patent US 6093561.
ACCESSION AR104347
VERSION AR104347.1 GI:12817055
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1486)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lysophospholipase
JOURNAL Patent: US 6093561-A 4 25-JUL-2000;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 99.8%; Score 708.4; DB 6; Length 1486;
Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGTCACATGTCACCCCGCTGCCCGCATCGTGCCTCCCGCCGCGAAGGCC 60
DB 76 ATGTGCGGCAATAAATGTCACATGTCACCCCGCTGCCCGCATCGTGCCTCCCGCCGCGAAGGCC 135

QY 61 ACCGCTGCGGTGATTTTCTGTCATGATTTGGGAGATCTGGGCACGGATGGGCGAAGGCC 120
DB 136 ACCGCTGCGGTGATTTTCTGTCATGATTTGGGAGATCTGGGCACGGATGGGCGAAGGCC 195

QY 121 TTTCAGAGTATCAGAGTTTACATATCAATATATCTGCCCGCATCGCTGTAGGCCT 180
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QY 181 GTTACATTAATAATGAACGTGGCTATGCTTTCATGTTTGTATATTTGGGCTTTTCACCA 240
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QY 241 GATTTCACAGAGATGAATCTGGGATTTAAACAGGACGAGAAAATAATAAAGCTTTTGATT 300
DB 316 GATTTCACAGAGATGAATCTGGGATTTAAACAGGACGAGAAAATAATAAAGCTTTTGATT 375

QY 301 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATATTTTGGAGGGTTTCTCAG 360
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QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACACAGCAGAAATCGGCAGTGTCACT 420
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QY 421 GCACCTCAGTTGCTGGCTTCCACTTTCGAGTTCCTTCCACAGGGTCTTATCGGTGGTCT 480
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QY 481 AATAGAGATATTTCTATTTCCAGTGCACGGGATTTGACCCCTTTGGTTCCCTCGATG 540
DB 556 AATAGAGATATTTCTATTTCCAGTGCACGGGATTTGACCCCTTTGGTTCCCTCGATG 615

QY 541 TTTGGTTCTTACGGTGGAAAACCTAAACAACTTGGTGAATCCAGCCATGTGACCTTT 600
DB 616 TTTGGTTCTTACGGTGGAAAACCTAAACAACTTGGTGAATCCAGCCATGTGACCTTT 675

QY 601 AAAACCTATGAAGTATGATGCACAGTTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 660
DB 676 AAAACCTATGAAGTATGATGCACAGTTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 735

QY 661 TTCATTGATAAATCTCTACCTCAATTTGATTGACGTCACTAAGAGGCCTT 710
DB 736 TTCATTGATAAATCTCTACCTCAATTTGATTGACGTCACTAAGAGGCCTT 785

RESULT 7
BD191690
LOCUS Human lysophospholipase.
DEFINITION BD191690
ACCESSION BD191690
VERSION JP 2002514081-A/2.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1486)
AUTHORS Hillman, J.L., Shah, P. and Murry, L.E.
TITLE Human lysophospholipase
JOURNAL Patent: JP 2002514081-A 2 14-MAY-2002;
INCYTE PHARMACEUTICALS INC
COMMENT PN JP 2002514081-A/2
PF 14-MAY-2002
PD 29-APR-1998 JP 1998547407
PR 29-APR-1997 US 08/844120, 12-FEB-1998 US 09/022940 PI
JENNIFER L HILLMAN, PURVI SHAH, LYNN E MURRY
PC C12N15/55, C12N9/18, A61K38/46, C07K16/40, C12Q1/68 CC
FH Key Location/Qualifiers.
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source 1. 1486
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 99.8%; Score 708.4; DB 6; Length 1486;
Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGCGGCAATAACATGTCACACCGCGTGCCTCCCGCCATCGTCCCGCCGCGCGCGGAGGCC 60
DB 76 ATGTGCGGCAATAACATGTCACACCGCGTGCCTCCCGCCATCGTCCCGCCGCGCGGAGGCC 135
QY 61 ACCGCTGGGTGATTTCTCGATGATGTTGGAGATCTGGGCACGGATGGCAGAGCC 120
DB 136 ACCGCTGGGTGATTTCTCGATGATGTTGGAGATCTGGGCACGGATGGCAGAGCC 195
QY 121 TTTTCAGGTATCAGAGTTTACATATCAATATATCTGCCCGATCGCGCTGTAGGCCT 180
DB 196 TTTCAGGTATCAGAGTTTACATATCAATATATCTGCCCGATCGCGCTGTAGGCCT 255
QY 181 GTTACATTAATAATGAACGTGCTATGCCTTCATGTTTGATATATTATTTGGGCTTTTCAACA 240
DB 256 GTTACATTAATAATGAACGTGCTATGCCTTCATGTTTGATATATTATTTGGGCTTTTCAACA 315
QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGACGACGAGAAATATAAAGCTTTGATT 300
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QY 301 GATCAGAGTCAAGATGGCATTCCTCTAACAGAAATATTATTTGGAGGGTTTCTCAG 360
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QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACCACACAGCAGAAACTGGCAGGTGTCACT 420
DB 436 GGAGGAGCTTTATCTTTATATATCTGCTTACCACACAGCAGAAACTGGCAGGTGTCACT 495
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTTCCACAGGTCCTATCGGTGGTCT 480
DB 496 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTTCCACAGGTCCTATCGGTGGTCT 555
QY 481 AATAGAGATATTCTATTCTCCAGTCCACGGGATTTGACCCCTTTGGTTCCCTCGATG 540
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QY 601 AAAACCTATGAAGGTATGATGACAGTTCTGTTCAACAGGAAATGATGATGTCAGCAA 660
DB 676 AAAACCTATGAAGGTATGATGACAGTTCTGTTCAACAGGAAATGATGATGTCAGCAA 735
QY 661 TTTCATTGATAAACTCCTACCTCAATTTGATTGACGTCACCTAAGAGCCCTT 710
DB 736 TTTCATTGATAAACTCCTACCTCAATTTGATTGACGTCACCTAAGAGCCCTT 785

RESULT 8

AR203099
LOCUS AR203099 1556 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 18 from patent US 6365354.
ACCESSION AR203099
VERSION AR203099.1 GI:21499401
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1556)
AUTHORS Bennett, C. Frank. and Wyatt, J.
TITLE Antisense modulation of lysophospholipase I expression
JOURNAL Patent: US 6365354-A 18 02-APR-2002;
FEATURES
source 1. 1556
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 99.8%; Score 708.4; DB 6; Length 1556;
Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGCGGCAATAACATGTCACACCGCGTGCCTCCCGCCATCGTCCCGCCGCGCGGAGGCC 60
DB 195 ATGTGCGGCAATAACATGTCACACCGCGTGCCTCCCGCCATCGTCCCGCCGCGCGGAGGCC 254
QY 61 ACCGCTGGGTGATTTCTCGATGATGTTGGAGATCTGGGCACGGATGGCAGAGCC 120
DB 255 ACCGCTGGGTGATTTCTCGATGATGTTGGAGATCTGGGCACGGATGGCAGAGCC 314
QY 121 TTTTCAGGTATCAGAGTTTACATATCAATATATCTGCCCGATCGCGCTGTAGGCCT 180
DB 315 TTTTCAGGTATCAGAGTTTACATATCAATATATCTGCCCGATCGCGCTGTAGGCCT 374
QY 181 GTTACATTAATAATGAACGTGCTATGCCTTCATGTTTGATATATTATTTGGGCTTTTCAACA 240
DB 375 GTTACATTAATAATGAACGTGCTATGCCTTCATGTTTGATATATTATTTGGGCTTTTCAACA 434
QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGACGACGAGAAATATAAAGCTTTGATT 300
DB 435 GATTCACAGGAGATGAATCTGGGATTAACAGGACGACGAGAAATATAAAGCTTTGATT 494
QY 301 GATCAGAGTCAAGATGGCATTCCTCTAACAGAAATATTATTTGGAGGGTTTCTCAG 360
DB 495 GATCAGAGTCAAGATGGCATTCCTCTAACAGAAATATTATTTGGAGGGTTTCTCAG 554
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACCACACAGCAGAAACTGGCAGGTGTCACT 420
DB 555 GGAGGAGCTTTATCTTTATATATCTGCTTACCACACAGCAGAAACTGGCAGGTGTCACT 614
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTTCCACAGGTCCTATCGGTGGTCT 480
DB 615 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTTCCACAGGTCCTATCGGTGGTCT 674
QY 481 AATAGAGATATTCTATTCTCCAGTCCACGGGATTTGACCCCTTTGGTTCCCTCGATG 540
DB 675 AATAGAGATATTCTATTCTCCAGTCCACGGGATTTGACCCCTTTGGTTCCCTCGATG 734
QY 541 TTTGGTTCTCTTACGGTGGAAAACTAAAAAATTTGGTGAATCCAGCCAAATGTGACCTTT 600
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DB 795 AAAACCTATGAAGGTATGATGACAGTTCTGTTCAACAGGAAATGATGATGTCAGCAA 854
QY 661 TTTCATTGATAAACTCCTACCTCAATTTGATTGACGTCACCTAAGAGCCCTT 710
DB 855 TTTCATTGATAAACTCCTACCTCAATTTGATTGACGTCACCTAAGAGCCCTT 904

RESULT 9

AF052112 1556 bp mRNA linear PRI 05-AUG-1998
LOCUS Homo sapiens clone 23753 mRNA sequence.
ACCESSION AF052112
VERSION AF052112.1 GI:3360419
FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1556)
Andersson,B., Wentland,M.A., Ricafrente,J.Y., Liu,W. and Gibbs,R.A.
A 'double adaptor' method for improved shotgun library construction
Anal. Biochem. 236 (1), 107-113 (1996)
8619474
PUBMED
2 (bases 1 to 1556)
Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W.,
Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
Large-scale concatenation cDNA sequencing
Genome Res. 7 (4), 353-358 (1997)
9110174
PUBMED
3 (bases 1 to 1556)
Yu,W., Sarginson,J. and Gibbs,R.A.
Direct Submission
Submitted (05-MAR-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
Location/Qualifiers
1. .1556
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/db_xref="taxon:9606"
/clone="I.M.A.G.E. Consortium clone ID 23753"
/sex="female"
/tissue_type="brain"
/clone_lib="INIB"
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encoded by GenBank Accession Number AF035293"

FEATURES
source
Query Match 99.8%; Score 708.4; DB 8; Length 1556;
Best Local Similarity 99.9%; Pred. No. 1.5e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGGGCAATTAACATGTCACCCCGCTCCCGCCATCTGTGCGCGCCCGCCCGCCCGGAGGCC 60
DB 195 ATGTGGGCAATTAACATGTCACCCCGCTCCCGCCATCTGTGCGCGCCCGCCCGCCCGGAGGCC 254
QY 61 ACCGCTGCGGTGATTTCTTCGATGTTGGAGATCTGGGACGATGGGAGGCC 120
DB 255 ACCGCTGCGGTGATTTCTTCGATGTTGGAGATCTGGGACGATGGGAGGCC 314
QY 121 TTTCAGGATCAGAGTTCACATATCAATATATCTGCCCGATGCGCCTGTAGGCCT 180
DB 315 TTTCAGGATCAGAGTTCACATATCAATATATCTGCCCGATGCGCCTGTAGGCCT 374
QY 181 GTTACATTAATATGAACGTGGGTATGCCCTTCATGTTGATATTTAGGCTTTACCA 240
DB 375 GTTACATTAATATGAACGTGGGTATGCCCTTCATGTTGATATTTAGGCTTTACCA 434
QY 241 GATTTCAGAGGATGATCTGGGATTAACAGCGCAGCAAAATATAAAGCTTTGATT 300
DB 435 GATTTCAGAGGATGATCTGGGATTAACAGCGCAGCAAAATATAAAGCTTTGATT 494
QY 301 GATCAAGAGTGAAGATGGCATCTCTTAAACAGAAATTTTGGAGGGTTTCTCAG 360
DB 495 GATCAAGAGTGAAGATGGCATCTCTTAAACAGAAATTTTGGAGGGTTTCTCAG 554
QY 361 GGAGGAGCTTTATCTTTATATCTGCGCTTTACCAACAGCAGAAATCGGAGGTGCACT 420
DB 555 GGAGGAGCTTTATCTTTATATCTGCGCTTTACCAACAGCAGAAATCGGAGGTGCACT 614

QY 421 GCACCTCAGTTCGTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTCT 480
DB 615 GCACCTCAGTTCGTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTCT 674
QY 481 AATAGAGATATTTCTTATTTCTCAGTGCACCGGGATTTGTGACCCCTTTGGTTCCCTGTATG 540
DB 675 AATAGAGATATTTCTTATTTCTCAGTGCACCGGGATTTGTGACCCCTTTGGTTCCCTGTATG 734
QY 541 TTTCAGGATCAGAGTTCACATATCAATATATCTGCCCGATGCGCCTGTAGGCCT 600
DB 735 TTTCAGGATCAGAGTTCACATATCAATATATCTGCCCGATGCGCCTGTAGGCCT 794
QY 601 AAAAAGCTATGAAGTATGATGACAGTTCGTGCAACAGCAAAATGATGATGTCAGCAAGCAA 660
DB 795 AAAAAGCTATGAAGTATGATGACAGTTCGTGCAACAGCAAAATGATGATGTCAGCAAGCAA 854
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DB 855 TTTCAGGATCAGAGTTCACATATCAATATGATGACGTCACCTAAGAGGCCCTT 904
RESULT 10
CQ894709 2417 bp DNA linear PAT 05-NOV-2004
LOCUS Sequence 19 from Patent EP1471075.
DEFINITION CQ894709
ACCESSION CQ894709
VERSION CQ894709.1 GI:55467458
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1
Rosenthal,A.D., Pillarsky,C., Dahl,E., Specht,T., Bruemendorf,T.,
Lichner,R., Staub,E., Roepcke,S. and Li,X.I.
Human nucleic acid sequences expressed in pancreatic carcinomas
Patent: EP 1471075-A 19 27-OCT-2004;
Hinzmann, Bernd (DE); Rosenthal, Andre (DE); Pillarsky, Christian
(DE); Dahl, Edgar (DE); Specht, Thomas (DE); Lichtner, Rosemarie
(DE)
FEATURES
Location/Qualifiers
1. .2417
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Query Match 99.8%; Score 708.4; DB 6; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.6e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGGGCAATTAACATGTCACCCCGCTCCCGCCATCTGTGCGCGCCCGCCCGGAGGCC 60
DB 36 ATGTGGGCAATTAACATGTCACCCCGCTCCCGCCATCTGTGCGCGCCCGCCCGGAGGCC 95
QY 61 ACCGCTGCGGTGATTTCTTCGATGTTGGAGATCTGGGACGATGGGAGGCC 120
DB 96 ACCGCTGCGGTGATTTCTTCGATGTTGGAGATCTGGGACGATGGGAGGCC 155
QY 121 TTTCAGGATCAGAGTTCACATATCAATATATCTGCCCGATGCGCCTGTAGGCCT 180
DB 156 TTTCAGGATCAGAGTTCACATATCAATATATCTGCCCGATGCGCCTGTAGGCCT 215
QY 181 GTTACATTAATATGAACGTGGGTATGCCCTTCATGTTGATATTTAGGCTTTACCA 240
DB 216 GTTACATTAATATGAACGTGGGTATGCCCTTCATGTTGATATTTAGGCTTTACCA 275
QY 241 GATTTCAGAGGATGATCTGGGATTAACAGCGCAGCAAAATATAAAGCTTTGATT 300
DB 276 GATTTCAGAGGATGATCTGGGATTAACAGCGCAGCAAAATATAAAGCTTTGATT 335
QY 301 GATCAAGAGTGAAGATGGCATCTCTTAAACAGAAATTTTGGAGGGTTTCTCAG 360


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Db      216 GTTACATTAATATGAACGTGGCTATGCGCTTCATGGTTTGATATATTATCGGGCTTTCACCA 275
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QY      361 GGAGGAGCTTTATCTTTATATATCTGCTTACCACAGCAGAAACTGGCAGGTGCACCT 420
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QY      421 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCCTATCGGTGGTCT 480
Db      456 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCCTATCGGTGGTCT 515
QY      481 AATAGAGATATTCTATTCTCCAGTCCACGGGATTTGACCCCTTTGGTTCCCTCGATG 540
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QY      541 TTTGGTTCTTACGGTGGAATACTAAACATTTGGTGAATCCAGCCCAATGTGACCTTT 600
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RESULT 13
AX256070 LOCUS 2417 bp DNA linear PAT 10-OCT-2001
Sequence 221 from Patent WO0170976.
AX256070 DEFINITION
AX256070 Homo sapiens (human)
AX256070.1 GI:16075110
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Xu,J., Pyle,R.A. and Stolk,J.A.
TITLE Compositions and methods for the therapy and diagnosis of ovarian
and endometrial cancer
JOURNAL Patent: WO 0170976-A 221 27-SEP-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1 .2417
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ORIGIN
Query Match 99.8%; Score 708.4; DB 6; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.6e-190;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGGGGCAATACATGTCAACCCCGCTCGCCGCATCGTCCGCCCGCCCGGAGGCC 60
Db 36 ATGTGGGGCAATACATGTCAACCCCGCTCGCCGCATCGTCCGCCCGCCCGGAGGCC 95
QY 61 ACCGCTCGGTGATTTTCTGATGATTCGGAGATCTGGCAGCATGGCAGGAGGCC 120
Db 96 ACCGCTCGGTGATTTTCTGATGATTCGGAGATCTGGCAGCATGGCAGGAGGCC 155
QY 121 TTTGCAGGTATCAGAAAGTTCACATATCAAAATATATCTGCCCGCATGCGCCTGTAGGCCCT 180
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QY      241 GATTCACAGGAGGATGAATCTGGGATTAAACAGGAGCAGAGAAATAATAAAGCTTTGATT 300
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QY      301 GATCAAGAAAGTGAAGAAATGGCAATCTCTTAACAGAAATATTATTTGGAGGGTTTCTCAG 360
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QY      541 TTTGGTTCTTACGGTGGAATACTAAACATTTGGTGAATCCAGCCCAATGTGACCTTT 600
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QY      601 AAAACCTATGAGGTATGATGACAGTTGCTGTCACAGGAATGATGATGTCAGCA 660
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QY      661 TTCATTGATAAACTCCTACCTCAATTTGATTGACGTCACTAAGAGCCCTT 710
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RESULT 14
AF081281 LOCUS 2417 bp mRNA linear PRI 13-AUG-1998
Homo sapiens lysophospholipase (LPL1) mRNA, complete cds.
AF081281 DEFINITION
AF081281 Homo sapiens
AF081281.1 GI:3415122
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 2417)
Hu,G.
Direct Submission
TITLE Submitted (02-AUG-1998) Shanghai Institute of Cell Biology, 320
JOURNAL Yue-Yang Road, Shanghai 200031, China
FEATURES
source Location/Qualifiers
1 .2417
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/genes="LPL1"
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ORIGIN	Query Match Best Local Similarity 99.8%; Score 708.4; DB 8; Length 2417; Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCCGCGGAGGCC 60
Db	36 ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCCGCGGAGGCC 95
QY	61 ACCGCTGCGGTGATTTTCTGTCATGATGGAGATACCTGGGACGAGATGGGAGGCC 120
Db	96 ACCGCTGCGGTGATTTTCTGTCATGATGGAGATACCTGGGACGAGATGGGAGGCC 155
QY	121 TTTCAGAGTATCAGAAAGTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 180
Db	156 TTTCAGAGTATCAGAAAGTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 215
QY	181 GTTACATTAATATGAACGTGGCTATGCCCTTCATGCTTTGATATTAATTTGGCT 240
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QY	241 GATTCACAGAGGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 300
Db	276 GATTCACAGAGGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 335
QY	301 GATCAAGAGTGAAGATGGCATCTTCTAAGAAATTAATTTGGGAGGTTTCTCAG 360
Db	336 GATCAAGAGTGAAGATGGCATCTTCTAAGAAATTAATTTGGGAGGTTTCTCAG 395
QY	361 GGAGGAGCTTATCTTTATATCTGCTTACCACAGCAGAGAACTGGCAGGTGCACT 420
Db	396 GGAGGAGCTTATCTTTATATCTGCTTACCACAGCAGAGAACTGGCAGGTGCACT 455
QY	421 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGCT 480
Db	456 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGCT 515
QY	481 AATAGAGATATTCTATTCTCAGTCCACGGGATTTGACCCCTTTGGTTCCCTGATG 540
Db	516 AATAGAGATATTCTATTCTCAGTCCACGGGATTTGACCCCTTTGGTTCCCTGATG 575
QY	541 TTGTGTTCTTACGCTGGAAACTTAAACATTTGGTGAATCCAGCCCATGTGACCTTT 600
Db	576 TTGTGTTCTTACGCTGGAAACTTAAACATTTGGTGAATCCAGCCCATGTGACCTTT 635
QY	601 AAAACCTATGAGGTATGATGCACAGTTGCTGTCAACAGGAAATGATGGATGTCAAGCAA 660
Db	636 AAAACCTATGAGGTATGATGCACAGTTGCTGTCAACAGGAAATGATGGATGTCAAGCAA 695
QY	661 TTCAATTGATAAACTCCTACCTCAATTTGATGACGTCACTAAGAGGCTTT 710
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RESULT 15
CQ493329
LOCUS
Sequence 25196 from Patent WO0160860.
DEFINITION
CQ493329
ACCESSION
CQ493329.1 GI:41458948
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1
AUTHORS
TITLE
Schlegel, R., Endege, W.O. and Monahan, J.E.
Genes differentially expressed in human prostate cancer and their use

JOURNAL Patent: WO 0160860-A 25196 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)

FEATURES
Source
1..2600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match Best Local Similarity 99.9%; Score 708.4; DB 6; Length 2600; Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	QY	1 ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCCGCGGAGGCC 60
	Db	163 ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCCGCGGAGGCC 222
	QY	61 ACCGCTGCGGTGATTTTCTGTCATGATGGAGATACCTGGGACGAGATGGGAGGCC 120
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	QY	121 TTTCAGAGTATCAGAAAGTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 180
	Db	283 TTTCAGAGTATCAGAAAGTTCAATATCAATATATCTGCCCGCATCGCTGTAGGCT 342
	QY	181 GTTACATTAATATGAACGTGGCTATGCCCTTCATGCTTTGATATTAATTTGGCT 240
	Db	343 GTTACATTAATATGAACGTGGCTATGCCCTTCATGCTTTGATATTAATTTGGCT 402
	QY	241 GATTCACAGGAGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 300
	Db	403 GATTCACAGGAGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 462
	QY	301 GATCAAGAGTCAAGATGGCATCTTCTTAACAGAAATTAATTTGGGAGGTTTCTCAG 360
	Db	463 GATCAAGAGTCAAGATGGCATCTTCTTAACAGAAATTAATTTGGGAGGTTTCTCAG 522
	QY	361 GGAGGAGCTTTATCTTTATATATCTGCCCTTACCACAGCAGAGAACTGGCAGGTGCACT 420
	Db	523 GGAGGAGCTTTATCTTTATATATCTGCCCTTACCACAGCAGAGAACTGGCAGGTGCACT 582
	QY	421 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGCT 480
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	QY	481 AATAGAGATATTCTATTCTCCAGTCCACGGGATTTGACCCCTTTGGTTCCCTGATG 540
	Db	643 AATAGAGATATTCTATTCTCCAGTCCACGGGATTTGACCCCTTTGGTTCCCTGATG 702
	QY	541 TTGTGTTCTTACCGTGGAAAACTAAAAACATTTGGTGAATCCAGCCCATGTGACCTTT 600
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	QY	601 AAAACCTATGAGGTATGATGCACAGTTGCTGTCAACAGGAAATGATGATGTCAAGCAA 660
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	QY	661 TTCAATTGATAAACTCCTACCTCAATTTGATGACGTCACTAAGAGGCTTT 710
	Db	823 TTCAATTGATAAACTCCTACCTCAATTTGATGACGTCACTAAGAGGCTTT 872

Search completed: April 14, 2006, 13:35:37
Job time : 3815 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:17:45 ; Search time 587 Seconds
(without alignments)
8061.213 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
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10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	710	100.0	758	AAH26336	Human bra
2	708.4	99.8	1348	ADP81609	Adf81609 Leukaemia
3	708.4	99.8	1486	AAH56267	Human lys
4	708.4	99.8	1486	ACC82267	Human NOV
5	708.4	99.8	1486	ADT71491	Human lys
6	708.4	99.8	1556	ABK37045	DNA encod
7	708.4	99.8	2415	ADQ87736	Human tum
8	708.4	99.8	2417	AAH56597	Human cdn
9	708.4	99.8	2417	ABK37030	DNA encod
10	708.4	99.8	2417	ABL59514	Human lys
11	708.4	99.8	2417	ADR65833	Human pro
12	708.4	99.8	2417	ADR66517	Human pro
13	708.4	99.8	2417	ADX97471	Pancreat
14	708.4	99.8	2493	AAH98208	Human col
15	708.4	99.8	2578	ACN38804	Tumour-as
16	708.4	99.8	2600	ABV5207	Human pro
17	686.4	96.7	1538	AAH71464	DNA encod
18	668.4	94.1	701	ACC62265	Human NOV
19	668.4	94.1	701	ADH47693	Human NOV

20	668.4	94.1	701	12	ADJ78963	Adj78963 Human NOV
21	604.4	85.1	2417	8	ACC49478	Acc49478 Human lys
22	602.8	84.9	2467	10	ADF81763	Adf81763 Leukaemia
23	602.4	84.8	1300	3	AAZ61501	Aaz61501 cDNA enco
24	565	79.6	693	6	ABK37037	Abk37037 DNA enco
25	565	79.6	2396	4	AAH34424	Aah34424 Human col
26	556.4	78.4	727	6	ABK37048	Abk37048 DNA enco
27	552.8	77.9	709	2	AAH56266	Aah56266 Human lys
28	495.2	69.7	521	14	ADV74708	Adv74708 Human col
29	408.8	57.6	616	8	ACC62266	Acc62266 Human NOV
30	404.6	57.0	419	6	ABL37780	AbL37780 Human col
31	397.4	56.0	470	14	ADV74570	Adv74570 Human col
32	343.4	48.4	441	8	ABX38759	Abx38759 Bovine ES
33	337.2	47.5	662	13	ADQ54630	Adq54630 Novel can
34	315.4	44.4	576	14	ACL56531	AcL56531 Human col
35	282.4	39.8	1536	10	ADB53247	Abd53247 Primary r
36	277.6	39.1	1622	12	ADQ87643	Adq87643 Human tum
37	277.6	39.1	1624	4	AAH56229	Aah56229 Human hyd
38	277.6	39.1	1624	10	ADB90836	AdB90836 Human CDN
39	277.6	39.1	1625	10	ADH61157	Adh61157 Human hyd
40	277.6	39.1	1647	6	ABL59535	AbL59535 Human lys
41	277.6	39.1	1648	13	ACN37299	Acn37299 Tumour-as
42	263.2	37.1	1624	12	ADQ83757	Adq83757 Human tum
43	263.2	37.1	1624	13	ACN38429	Acn38429 Tumour-as
44	200.2	28.2	1061	13	ADQ83758	Adq83758 Human tum
45	200.2	28.2	1061	13	ACN38433	Acn38433 Tumour-as

ALIGNMENTS

RESULT 1
AAH26336

ID AAH26336 standard; cdna; 758 BP.

AC AAH26336;

DT -02-OCT-2001 (first entry)

XX Human brain lysophospholipase cDNA.

XX Lysophospholipase; human; brain; lysophospholipid; atherosclerosis;
XX hyperlipidaemia; dysrhythmia; myocardial ischaemia; demyelination;
XX vasotropic; antiatherosclerotic; antilipaeamic; neuroprotective;
XX gene therapy; LysoPLA; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
CDS 49..741

FT /*tag= a

FT /note= "the coding region from position 48 to position

741 is specifically claimed in Claim 1"

FT complement(49..74)

FT /*tag= b

FT primer_bind 716..741

FT primer_bind /*tag= c

WO200155166-A1.

02-AUG-2001.

28-JAN-2000; 2000WO-US002319.

28-JAN-2000; 2000US-00493601.

(REGC) UNIV CALIFORNIA.

Dennis EA, Wang A;

WPI; 2001-483215/52.

P-PSDB; AAB82669.

XX


```
QY 121 TTTGCAAGGTATCAGAAAGTTTCACATATCAAAATATATCTGCCCGCATCGCGCTGTAGGCTT 180
DB 126 TTTGCAAGGTATCAGAAAGTTTCACATATCAAAATATATCTGCCCGCATCGCGCTGTAGGCTT 185
QY 181 GTTACATTAAATATGAACGTGGCTATGCTTCATGTTTGATATATTTGGGCTTTTCACCA 240
DB 186 GTTACATTAAATATGAACGTGGCTATGCTTCATGTTTGATATATTTGGGCTTTTCACCA 245
QY 241 GATTTCACAGGAGGATGAATCTGGGATTAAACAGGCAGCAGAAATAATAAAGCTTTGATT 300
DB 246 GATTTCACAGGAGGATGAATCTGGGATTAAACAGGCAGCAGAAATAATAAAGCTTTGATT 305
QY 301 GATCAAGAAGTGAAGATGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 360
DB 306 GATCAAGAAGTGAAGATGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 365
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGCAGAACTGGCAGGTGTCAC 420
DB 366 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGCAGAACTGGCAGGTGTCAC 425
QY 421 GCACCTCAGTTGCTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGGTCT 480
DB 426 GCACCTCAGTTGCTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGGTCT 485
QY 481 AATAGAGATATTTCTATCTCAGTGCACGGGATGTGACCCCTTTGGTTCCCTCGATG 540
DB 486 AATAGAGATATTTCTATCTCAGTGCACGGGATGTGACCCCTTTGGTTCCCTCGATG 545
QY 541 TTTGGTTCTTACGCTGGAAACCTAAACAACTTGGTGAATCCAGCCATGTGACCTTT 600
DB 546 TTTGGTTCTTACGCTGGAAACCTAAACAACTTGGTGAATCCAGCCATGTGACCTTT 605
QY 601 AAAACCTATCAAGGTATGATGCACAGTTCTGTGTCACAGGAATGATGGATGTCAAGCAA 660
DB 606 AAAACCTATCAAGGTATGATGCACAGTTCTGTGTCACAGGAATGATGGATGTCAAGCAA 665
QY 661 TTCATTGATAAACTCTTACCTCAATTTGATGACGTCACTAAGAGGCTTT 710
DB 666 TTCATTGATAAACTCTTACCTCAATTTGATGACGTCACTAAGAGGCTTT 715

RESULT 3
AA56267
ID AAX56267 standard; cDNA; 1486 BP.
AC AAX56267;
XX
XX
DT 19-JUL-1999 (first entry)
DE Human lysophospholipase extended NHLP encoding cDNA.
XX
XX Human; lysophospholipase; NHLP: cell proliferation; arteriosclerosis;
KW arteriosclerosis; bursitis; cirrhosis; hepatitis; myelofibrosis;
KW mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;
KW polycythaemia vera; psoriasis; primary thrombocytopenia; cancer;
KW inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;
KW immune response; ankylosing spondylitis; autoimmune haemolytic anaemia;
KW ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 76..768
XX FT /*tag= a
XX FT /product= "NHLP"
XX
XX MO9849319-A1.
XX
XX PD 05-NOV-1998.
XX
XX PF 29-APR-1998; 98WO-US0008782.
XX
XX PR 29-APR-1997; 97US-00844120.
```

```
PR 12-FEB-1998; 98US-00022940.
XX (INCY-) INCYTE PHARM INC.
XX Hillman JL, Shah P, Murry LE;
XX WPI; 1999-326512/27.
DR P-PSDB; AAY09531.
XX
XX New human lysophospholipase (NHLP) polypeptides and polynucleotides which
XX identify and encode NHLP.
XX
XX Claim 7; Fig 2; 66pp; English.
XX
XX The present sequence encodes human lysophospholipase (NHLP). The present
XX invention also describes a method for treating or preventing a disorder
XX of cell proliferation (e.g. arteriosclerosis, atherosclerosis, bursitis,
XX cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis,
XX paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis,
XX primary thrombocytopenia, and cancers), inflammation (e.g. Addison's
XX disease, AIDS, allergies, asthma, atherosclerosis, bronchitis) and a
XX disorder of the immune response (e.g. AIDS, allergies, ankylosing
XX spondylitis, autoimmune haemolytic anaemia) by administering an
XX antagonist to NHLP. NHLP proteins, antagonists, antibodies, agonists,
XX complementary sequences or vectors may be administered in combination
XX with other therapeutic agents. Antibodies which specifically bind to NHLP
XX may be used for the diagnosis of disorders characterized by expression of
XX NHLP or in assays to monitor patients being treated with NHLP or
XX agonists. The polynucleotides (PNS) encoding NHLP or fragments may be
XX used therapeutically. In one aspect, the complement of the
XX polynucleotides may be used where it would be desirable to block the
XX transcription of the mRNA. Complementary molecules may be used to
XX modulate NHLP activity or to achieve regulation of gene activity.
XX Diagnostically, the PNS may be used to detect and quantitate gene
XX expression in biopsied tissues in which expression of NHLP may be
XX correlated with disease
XX
XX SQ Sequence 1486 BP; 418 A; 304 C; 300 G; 459 T; 0 U; 5 Other;
XX
XX Query Match 99.8%; Score 708.4; DB 2; Length 1486;
XX Best Local Similarity 99.9%; Pred. No. 1.3e-221;
XX Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGCGGCAATAACATGTCACACCCCGCTGCCGCCATCGTGCCTCCCGCCCGAAGGCC 60
DB 76 ATGTGCGGCAATAACATGTCACACCCCGCTGCCGCCATCGTGCCTCCCGCCCGAAGGCC 135
QY 61 ACGCTGCGGTGATTTTCTCGATGGATTGGGAGATCTGGGCACGGATGGGCAGAGGCC 120
DB 136 ACGCTGCGGTGATTTTCTCGATGGATTGGGAGATCTGGGCACGGATGGGCAGAGGCC 195
QY 121 TTTGCAAGGTATCAGAAAGTTTCACATATCAAAATATATCTGCCCGCATCGCGCTGTAGGCTT 180
DB 196 TTTGCAAGGTATCAGAAAGTTTCACATATCAAAATATATCTGCCCGCATCGCGCTGTAGGCTT 255
QY 181 GTTACATTAAATATGAACGTGGCTATGCTTCATGTTTGATATATTTGGGCTTTTCACCA 240
DB 256 GTTACATTAAATATGAACGTGGCTATGCTTCATGTTTGATATATTTGGGCTTTTCACCA 315
QY 241 GATTTCACAGGAGGATGAATCTGGGATTAAACAGGCAGCAGAAATAATAAAGCTTTGATT 300
DB 316 GATTTCACAGGAGGATGAATCTGGGATTAAACAGGCAGCAGAAATAATAAAGCTTTGATT 375
QY 301 GATCAAGAAGTGAAGATGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 360
DB 376 GATCAAGAAGTGAAGATGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 435
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGCAGAACTGGCAGGTGTCAC 420
DB 436 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGCAGAACTGGCAGGTGTCAC 495
QY 421 GCACCTCAGTTGCTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGGTCT 480
```

Db 496 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTTCCACAGGGTCTTATCGTGGTGTCT 555
QY 481 AATAGAGATATTTCTATTCTTCAGTCCACGGGATTTGACCCCTTGGTTCCCTGTG 540
Db 556 AATAGAGATATTTCTATTCTTCAGTCCACGGGATTTGACCCCTTGGTTCCCTGTG 615
QY 541 TTTGGTTCTTACGGTGAAAAAATAAACAATTGGTGAATCCAGCCCAATGTGACCTTT 600
Db 616 TTTGGTTCTTACGGTGAAAAAATAAACAATTGGTGAATCCAGCCCAATGTGACCTTT 675
QY 601 AAAACCTATGAAGGTATGATGACACAGTTCGTGTCACAGGAATGATGATGTCAGCAA 660
Db 676 AAAACCTATGAAGGTATGATGACACAGTTCGTGTCACAGGAATGATGATGTCAGCAA 735
QY 661 TTCATTGATAAACTCTACTCTCAATGATTGACGTCACCTAAGAGCCCTT 710
Db 736 TTCATTGATAAACTCTACTCTCAATGATTGACGTCACCTAAGAGCCCTT 785

RESULT 4
ACC62267
ID ACC62267 standard; cDNA; 1486 BP.
XX
AC ACC62267;
AC
XX 23-JUN-2003 (first entry)
XX
XX Human NOV7c encoding cDNA SEQ ID NO:63.
DE
XX Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
KW anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaeamic;
KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW congenital heart defect; aortic stenosis; valve disease; transplantation;
KW tuberosus sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW fertility; haemophilia; hypercoagulation; graft versus host disease;
KW idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic syndrome X; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2003023001-A2.
XX
XX 20-MAR-2003.
XX
XX 09-SEP-2002; 2002WO-US028538.
XX
XX 07-SEP-2001; 2001US-0318120P.
XX 07-SEP-2001; 2001US-0318184P.
XX 10-SEP-2001; 2001US-0318430P.
XX 17-SEP-2001; 2001US-0322636P.
XX 17-SEP-2001; 2001US-0322781P.
XX 17-SEP-2001; 2001US-0322816P.
XX 17-SEP-2001; 2001US-0322817P.
XX 19-SEP-2001; 2001US-0323519P.
XX 19-SEP-2001; 2001US-0323611P.
XX 20-SEP-2001; 2001US-0323636P.
XX 25-SEP-2001; 2001US-0324969P.
XX 25-SEP-2001; 2001US-0325091P.
XX 26-SEP-2001; 2001US-0324990P.
XX 14-DEC-2001; 2001US-0341144P.
XX 26-FEB-2002; 2002US-0359599P.
XX 05-MAR-2002; 2002US-0361663P.
XX 03-MAY-2002; 2002US-0377908P.
XX 17-MAY-2002; 2002US-0381483P.
XX 29-MAY-2002; 2002US-0383863P.
XX 02-JUL-2002; 2002US-0393332P.
XX 17-JUL-2002; 2002US-0396412P.

PR 13-AUG-2002; 2002US-0403517P.
XX 06-SEP-2002; 2002US-00236417.
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
PI Crabtree J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K;
PI Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
PI Kekuda R, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
PI Malyankar UM, Miller CE, Ooi CE, Ort T, Padigar M, Patturajan M;
PI Pena CE, Rieger DK, Rothenberg MB, Shenoy SC, Shmkeles RA;
PI Spaderna SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ;
PI Zerhusen BD, Zhong M;
XX
XX WPI; 2003-313241/30.
DR P-PSDB; ABR54198.
XX
XX Novel human proteins and nucleic acid encoding the proteins, useful for
PT diagnosis, treatment and prevention of disorders involving the human
PT protein or nucleic acid e.g. cardiac and neurological disorders.
XX
XX Claim 20; Page 129-130; 460pp; English.
XX
XX The present invention describes isolated human NOVX proteins, where X is
CC 1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
CC hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
CC antidiabetic, antiinfertility, haemostatic, neuroprotective, anti-HIV,
CC antiasthmatic, metabolic, immunomodulator, antiparkinsonian, nootropic,
CC antiparkinsonian and antilipaeamic activities, and can be used in gene
CC therapy. NOVX proteins are useful for treating or preventing a pathology
CC associated with a NOVX protein in humans and for treating a syndrome
CC associated with the human disease. NOVX nucleic acids, proteins and
CC antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC valve disease, tuberosus sclerosis, scleroderma, obesity, transplantation,
CC congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC sequences, which are used in examples from the present invention.
CC ABR54277 represents a human crypsinogen protein given in comparison with
CC the human NOV35b protein in the exemplification of the present invention
XX
XX Sequence 1486 BP; 418 A; 304 C; 300 G; 459 T; 0 U; 5 Other:
SQ

Query Match 99.8%; Score 708.4; DB 8; Length 1486;
Best Local Similarity 99.9%; Pred. No. 1.3e-221;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGTCACCCCGCTGCCCGCCATCGTGCCTGCGGAGAGCC 60
Db 76 ATGTGCGGCAATAAATGTCACCCCGCTGCCCGCCATCGTGCCTGCGGAGAGCC 135
QY 61 ACCGCTGCGGTGATTTTCTGATGATTTGGGAGATCTGCGGACCGATGGGAGAGCC 120
Db 136 ACCGCTGCGGTGATTTTCTGATGATTTGGGAGATCTGCGGACCGATGGGAGAGCC 195
QY 121 TTTCAGGATATCAGAGTTTTCACATATCAATATCTGCCGATCGCTGTTAGGCGCT 180
Db 196 TTTCAGGATATCAGAGTTTTCACATATCAATATCTGCCGATCGCTGTTAGGCGCT 255
QY 181 GTTACATTAAATGAACGTGGCTATGCTTTCATGTTTTCATATTTAGGCTTTTACCA 240
Db 256 GTTACATTAAATGAACGTGGCTATGCTTTCATGTTTTCATATTTAGGCTTTTACCA 315
QY 241 GATTTCAGGAGATCAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTGATT 300

CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAR)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAR binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAR sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAR cDNA sequence from the present invention.

XX
SQ Sequence 2415 BP; 750 A; 414 C; 421 G; 830 T; 0 U; 0 Other;

Query Match 99.8%; Score 708.4; DB 12; Length 2415;
Best Local Similarity 99.9%; Pred. No. 1.7e-221;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 96 ACCGCTGCGGTGATTTTCTGCGATGATTTGGGAGATCTGGGCACCGATGGGAGGCC 155
QY 121 TTTCAGGTATCAGAGTTCACATATCAATATATCTGCCGATCGCTGTAGGCTT 180
DB 156 TTTCAGGTATCAGAGTTCACATATCAATATATCTGCCGATCGCTGTAGGCTT 215
QY 181 GTTACATTAATAATGAACGTGGCTATGCTTTCATGTTTATATTTGGGCTTTCCACCA 240
DB 216 GTTACATTAATAATGAACGTGGCTATGCTTTCATGTTTATATTTGGGCTTTCCACCA 275
QY 241 GATTTCAGAGGATGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTGATT 300
DB 276 GATTTCAGAGGATGAATCTGGGATTAACAGGACGAGAAATATAAAGCTTTGATT 335
QY 301 GATCAGAGTGAAGATGGCATTCCTTCTACAGAAATATTTTGGAGGGTTTCTCAG 360
DB 336 GATCAGAGTGAAGATGGCATTCCTTCTACAGAAATATTTTGGAGGGTTTCTCAG 395
QY 361 GGAGGAGCTTTATCTTTATATCTGCTTACACAGCAGAGAACTGGCAGGTGTCAC 420
DB 396 GGAGGAGCTTTATCTTTATATCTGCTTACACAGCAGAGAACTGGCAGGTGTCAC 455
QY 421 GCATCAGTTGCTGGCTTCCATTCGGGCTTCCCTTCCACAGGGTCTATTCGGTGTGCT 480
DB 456 GCATCAGTTGCTGGCTTCCATTCGGGCTTCCCTTCCACAGGGTCTATTCGGTGTGCT 515
QY 481 AATAGAGATTTTCTATCTCCAGTCCAGGGGATGTGACCTTTGGTTCCTCCCTGATG 540
DB 516 AATAGAGATTTTCTATCTCCAGTCCAGGGGATGTGACCTTTGGTTCCTCCCTGATG 575
QY 541 TTGTGTTCTCTACGGTGGAAAAAATAAATACTTGTGTAATCCAGCAATGTGACCTTT 600
DB 576 TTGTGTTCTCTACGGTGGAAAAAATAAATACTTGTGTAATCCAGCAATGTGACCTTT 635
QY 601 AAAACCTATGAAGGTATGATGTCAGTTCGTGTCAACAGGAAATGATGATGCAAGCAA 660

DB 636 AAAACCTATGAAGGTATGATGTCAGTTCGTGTCAACAGGAAATGATGATGTCAGCAA 695
QY 661 TTTCATTGATAAACTCCTACCTCCAAATGATTGATGACGTCAAGAGGCTTT 710
DB 696 TTTCATTGATAAACTCCTACCTCCAAATGATTGATGACGTCAAGAGGCTTT 745

RESULT 8

AAS56597
ID AAS56597 standard; cDNA; 2417 BP.

XX AAS56597;
AC
XX 18-DEC-2001 (first entry)
DT
XX Human cDNA for an ovarian cancer protein #221.
DE
XX Human; ss; ovarian cancer protein; cancer; tumour; ovarian cancer;
KW endometrial cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200170976-A2.
XX
PD 27-SEP-2001.
XX
XX 20-MAR-2001; 2001WO-US009062.
XX
XX 21-MAR-2000; 2000US-0190710P.
PR
XX 22-JUN-2000; 2000US-0213748P.
PR
XX 19-DEC-2000; 2000US-0257276P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Pyle RA, Stolk JA;
XX
XX WPI; 2001-607531/69.

XX Nucleic acids encoding 222 polypeptides associated with ovarian and
XX endometrial cancers, useful for diagnosing, preventing and treating
XX cancers.

XX Claim 1; Page 186-187; 187pp; English.

XX The invention relates to human polynucleotides encoding proteins
XX associated with ovarian and endometrial cancers. The polynucleotides and
XX the proteins they encode may be used in the prevention, diagnosis and
XX treatment of diseases associated with the inappropriate expression of
XX ovarian and endometrial cancer polypeptides (OECs). For example, the
XX polynucleotide (or an expression vector comprising the polynucleotide)
XX and the OEC may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of OECs by expressing inactive proteins or to
XX supplement the patients own production of them. Additionally, the
XX polynucleotide may be used to produce the OECs, by inserting the nucleic
XX acids into a host cell and culturing the cell to express the protein. The
XX polynucleotide and its complementary sequences may also be used as DNA
XX probes in diagnostic assays to detect and quantitate the presence of
XX similar nucleic acids in samples, and therefore which patients may be in
XX need of restorative therapy. The OECs may also be used as antigens in
XX the production of anti-OEC antibodies and in assays to identify
XX modulators of its expression and activity. The anti-OEC antibodies and
XX antagonists may also be used to down regulate expression and activity.
XX The anti-OEC antibodies may also be used as diagnostic agents for
XX detecting the presence of OEC in samples (e.g. by enzyme linked
XX immunosorbant assay (ELISA)) and hence diagnose patients with cancers.
XX The present sequence is a ovarian and endometrial cancer linked cDNA of
XX the invention

SQ Sequence. 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 U; 0 Other;

Query Match 99.8%; Score 708.4; DB 4; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.7e-221;

Query Match		99.8%;	Score 708.4;	DB 13;	Length 2417;
Best Local Similarity		99.9%;	Pred. No. 1.7e-221;		
Matches 709;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCCCGCCGGAAGGCC	60		
Db	36	ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCCCGCCGGAAGGCC	95		
Qy	61	ACCGCTGCGGTGATTTTCTGTCATGTGATTGGGAGATCTGGGCACGGATGGGCAGAAAGCC	120		
Db	96	ACCGCTGCGGTGATTTTCTGTCATGTGATTGGGAGATCTGGGCACGGATGGGCAGAAAGCC	155		
Qy	121	TTTGCAGGTATCAGAAATTCACATATCAAAATATATCTGCCCGCATCGCTGTAGGCCT	180		
Db	156	TTTGCAGGTATCAGAAATTCACATATCAAAATATATCTGCCCGCATCGCTGTAGGCCT	215		
Qy	181	GTTACATTAATAATGAAAGTGGCTTACCTTCATGTTTGAATATATTTGGGCTTTTCCACCA	240		
Db	216	GTTACATTAATAATGAAAGTGGCTTACCTTCATGTTTGAATATATTTGGGCTTTTCCACCA	275		
Qy	241	GATTACAGAGGATGAATCTGGGATTAAACAGGCAGACAGAAAATATAAAAGCTTTGATT	300		
Db	276	GATTACAGAGGATGAATCTGGGATTAAACAGGCAGACAGAAAATATAAAAGCTTTGATT	335		
Qy	301	GATCAAGAAGTGAAGATGGCATTCCTTCTAACAGAAATTAATTTGGGAGGGTTTTCTCAG	360		
Db	336	GATCAAGAAGTGAAGATGGCATTCCTTCTAACAGAAATTAATTTGGGAGGGTTTTCTCAG	395		
Qy	361	GGAGGAGCTTTATCTTTTATATCTGCCCTTACCACAGCAGAGAACTGGCAGGTGTCAC	420		
Db	396	GGAGGAGCTTTATCTTTTATATCTGCCCTTACCACAGCAGAGAACTGGCAGGTGTCAC	455		
Qy	421	GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGGTCCTATCGGTGGTCT	480		
Db	456	GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGGTCCTATCGGTGGTCT	515		
Qy	481	AATAGAGATATTCTTATTCTCCAGTGCCACGGGGAATGTGACCCCTTTGGTCCCTGATG	540		
Db	516	AATAGAGATATTCTTATTCTCCAGTGCCACGGGGAATGTGACCCCTTTGGTCCCTGATG	575		
Qy	541	TTTGGTTCCTTACGGTGGAATAAATAAATGATGGTGAATCCAGCCAAATGACCTTT	600		
Db	576	TTTGGTTCCTTACGGTGGAATAAATAAATGATGGTGAATCCAGCCAAATGACCTTT	635		
Qy	601	AAACCTATGAAGGTATGATGCACAGTTTCGTCTCAACAGGAAATGATGGATGTCAGCAA	660		
Db	636	AAACCTATGAAGGTATGATGCACAGTTTCGTCTCAACAGGAAATGATGGATGTCAGCAA	695		
Qy	661	TTCAATTGATAAACCCTTACCTCCAAATGATTGACGTCACTAAGAGGCCTT	710		
Db	696	TTCAATTGATAAACCCTTACCTCCAAATGATTGACGTCACTAAGAGGCCTT	745		
RESULT 14					
AAC98208					
ID	AAC98208 standard; cDNA; 2493 BP.				
XX					
AC	AAC98208;				
XX					
DT	09-MAR-2001 (first entry)				
XX					
DE	Human colon cancer antigen nucleotide sequence SEQ ID NO:218.				
XX					
KW	Human; colon cancer; colon cancer antigen; diagnosis; detection;				
KW	identification; cytostatic; cardioactive; neuroprotective; vulnary;				
KW	immunomodulatory; muscular; gynaecological; gastrointestinal;				
KW	nephrotropic; antiinfective; antibacterial; gene therapy; wound;				
KW	neural disorder; immune system disorder; muscular disorder;				
KW	reproductive disorder; gastrointestinal disorder; renal disorder;				
KW	infectious disease; cardiovascular disorder; ss.				
XX					
OS	Homo sapiens.				
XX					

PN	WO200055351-A1.				
XX					
PD	21-SEP-2000.				
XX					
PF	08-MAR-2000; 2000WO-US005883.				
XX					
PR	12-MAR-1999; 99US-0124270P.				
XX					
XX	(HUMA-) HUMAN GENOME SCI INC.				
XX					
PI	Rosen CA, Ruben SM;				
XX					
DR	WPI; 2000-587534/55.				
XX	P-PSDB; AAB53451.				
XX					
PT	Colon cancer associated gene sequences, referred to as colon cancer				
PT	antigens, useful for the treatment, prevention, and diagnosis of colon				
PT	disorders such as colon cancer.				
XX					
PS	Claim 1; Page 641; 2104pp; English.				
XX					
CC	AAC97991 to AAC98763 encode the human colon cancer associated proteins,				
CC	called human colon cancer antigens, given in AAB53234 to AAB54006. The				
CC	human colon cancer antigens can have cytostatic, cardioactive, muscular;				
CC	neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and				
CC	vulnary, nephrotropic, antiinfective and antibacterial activities, and				
CC	can be used in gene therapy. The colon cancer antigen polynucleotides,				
CC	proteins and antibodies to the proteins are useful for the prevention,				
CC	treatment and diagnosis of colon disorders, such as colon cancer. The				
CC	polynucleotides may be used in diagnostics and research, such as for				
CC	chromosome identification, and as hybridisation probes. The proteins may				
CC	also be used to prevent diseases such as neural disorders, immune system				
CC	disorders, muscular disorders, reproductive disorders, gastrointestinal				
CC	disorders, wounds, renal disorders, infectious diseases, and				
CC	cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent				
CC	sequences used in the exemplification of the present invention				
XX					
SQ	Sequence 2493 BP; 766 A; 442 C; 449 G; 836 T; 0 U; 0 Other;				
	Query Match	99.8%;	Score 708.4;	DB 3;	Length 2493;
	Best Local Similarity	99.9%;	Pred. No. 1.7e-221;		
	Matches 709;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCCCGCGAAGGCC	60		
Db	100	ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCCCGCGAAGGCC	159		
QY	61	ACCGCTGCGGTGATTTTCTGTCATGTGTTGGGAGATCTGGGCAGCGATGGGCAGAGCC	120		
Db	160	ACCGCTGCGGTGATTTTCTGTCATGTGTTGGGAGATCTGGGCAGCGATGGGCAGAGCC	219		
QY	121	TTTGCAGGTATCAGAAAGTTCCACATATCAAAATATATCTGCCCGCATCGCCTGTAGGCCT	180		
Db	220	TTTGCAGGTATCAGAAAGTTCCACATATCAAAATATATCTGCCCGCATCGCCTGTAGGCCT	279		
QY	181	GTTACATTAATAATGAACGTGCTATGCTTCATGGTTGATATTAATTTGGGCTTTTCACCA	240		
Db	280	GTTACATTAATAATGAACGTGCTATGCTTCATGGTTGATATTAATTTGGGCTTTTCACCA	339		
QY	241	GATTTCACAGGAGATGAATCTGGGATTAACAGGCAGCAGAAATATAAAGCTTTGATT	300		
Db	340	GATTTCACAGGAGATGAATCTGGGATTAACAGGCAGCAGAAATATAAAGCTTTGATT	399		
QY	301	GATCAAGAAGTGAAGATGGCATTCCTCTTAACAGAAATTAATTTGGGAGGGTTTCTCAG	360		
Db	400	GATCAAGAAGTGAAGATGGCATTCCTCTTAACAGAAATTAATTTGGGAGGGTTTCTCAG	459		
QY	361	GGAGGAGCTTTATCTTTTATATCTAGCCCTTACACAGAGAAATCGGAGGTGTCAC	420		
Db	460	GGAGGAGCTTTATCTTTTATATCTAGCCCTTACACAGAGAAATCGGAGGTGTCAC	519		
QY	421	GCACCTAGTGTGGCTTCCACTTCGGGCTTCCTTCCACAGGGTCTCTATCGGTGGTCT	480		

Db 520 GCACCTAGTTGCTGCCCTCCACTTCGGGGTCTCTTTCCACAGGGTCTATTCGGTGGTCT 579
 QY 481 AATAGAGATATTTCTATCTCCAGTGCACACGGGATTTGTGACCTTTTGGTTCCCTCGATG 540
 Db 580 AATAGAGATATTTCTATCTCCAGTGCACACGGGATTTGTGACCTTTTGGTTCCCTCGATG 639
 QY 541 TTTGGTCTCTTACGGTGAAACCTAAACCAATTGGTGAATCCAGCCAAATGTGACCTTT 600
 Db 640 TTTGGTCTCTTACGGTGAAACCTAAACCAATTGGTGAATCCAGCCAAATGTGACCTTT 699
 QY 601 AAACCTATGAGGTATGATGACAGTTCGTGTCAACAGGAATGATGATGTCAGCA 660
 Db 700 AAACCTATGAGGTATGATGACAGTTCGTGTCAACAGGAATGATGATGTCAGCA 759
 QY 661 TTCAATGATAAACTCTTACCTCCAAATTGATGACGTCACTAAGAGGCCTT 710
 Db 760 TTCAATGATAAACTCTTACCTCCAAATTGATGACGTCACTAAGAGGCCTT 809

RESULT 15

ACN38804

ID ACN38804 standard; cDNA; 2578 BP.

AC AC

AC AC

18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) cDNA DNAS25098, SEQ ID NO:2550.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic; gene; ss.

XX Homo sapiens.

XX WO2004030615-A2.

XX 15-APR-2004.

XX 29-SEP-2003; 2003WO-US028547.

XX 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

XX P-PSDB; ABM80990.

XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.

XX Claim 1; SEQ ID NO 2550; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful

CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention

SQ Sequence 2578 BP; 766 A; 472 C; 498 G; 842 T; 0 U; 0 Other;

Query Match 99.8%; Score 708.4; DB 13; Length 2578;

Best Local Similarity 99.9%; Pred. No. 1.8e-221;

Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGCAATAACATGTCAACCCGCTGCCCGCATCGTCCCGCCCGCGAAGGCC 60

Db 195 ATGTGCGCAATAACATGTCAACCCGCTGCCCGCATCGTCCCGCCCGCGAAGGCC 254

QY 61 ACCGTGCGGTGATTTCTGTCATGATTTGGGAGATCTGGGCACGGATGGCAGAGCC 120

Db 255 ACCGTGCGGTGATTTCTGTCATGATTTGGGAGATCTGGGCACGGATGGCAGAGCC 314

QY 121 TTTGCGGTATCAGAGTTTCAATATATCTGCCCGCATCGTCCCGCCCGCGAAGGCC 180

Db 315 TTTGCGGTATCAGAGTTTCAATATATCTGCCCGCATCGTCCCGCCCGCGAAGGCC 374

QY 181 GTTACATTAATAATGAACGTGCTATGCTTTCATGTTTGTATATTAATGCGCTTTCACCA 240

Db 375 GTTACATTAATAATGAACGTGCTATGCTTTCATGTTTGTATATTAATGCGCTTTCACCA 434

QY 241 GATTCAAGGAGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 300

Db 435 GATTCAAGGAGATGAATCTGGGATTAACAGGACAGAGAAATATAAAGCTTTGATT 494

QY 301 GATCAAGAGTCAAGATGCGCATTCCTCTCAACAGAAATATTATTTGGAGGGTTTCTCAG 360

Db 495 GATCAAGAGTCAAGATGCGCATTCCTCTCAACAGAAATATTATTTGGAGGGTTTCTCAG 554

QY 361 GGAGGAGCTTTATCTTTTATATATCTGCTTACCACACAGAGAACTGGCAGGTGTCACT 420

Db 555 GGAGGAGCTTTATCTTTTATATATCTGCTTACCACACAGAGAACTGGCAGGTGTCACT 614

QY 421 GCATCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGGTCT 480

Db 615 GCATCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGCTCTATCGGTGGTCT 674

QY 481 AATAGAGATATTTCTATTTCTCCAGTCCACGGGATTTGTGACCTTTTGGTTCCCTGTATG 540

Db 675 AATAGAGATATTTCTATTTCTCCAGTCCACGGGATTTGTGACCTTTTGGTTCCCTGTATG 734

QY 541 TTTGGTCTCTTACGGTGAAACCTAAAAACAATTGGTGAATCCAGCCAAATGTGACCTTT 600

Db 735 TTTGGTCTCTTACGGTGAAACCTAAAAACAATTGGTGAATCCAGCCAAATGTGACCTTT 794

QY 601 AAAACCTATCAAGGTATGATGACAGTTTGTGTCACAGGAAATGATGATGTCAGCAA 660

Db 795 AAAACCTATCAAGGTATGATGACAGTTTGTGTCACAGGAAATGATGATGTCAGCAA 854

QY 661 TTCAATGATAAACTCTTACCTCCAAATTGATGACGTCACTAAGAGGCCTT 710

Db 855 TTCAATGATAAACTCTTACCTCCAAATTGATGACGTCACTAAGAGGCCTT 904

Search completed: April 14, 2006, 14:01:06

Job time : 589 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:28:32 ; Search time 3943 Seconds

(without alignments)
8424.760 Million cell updates/sec

Title: US-09-493-601B-1

Perfect score: 710

Sequence: 1 atgtgcggcaataacatgtc.....tgacgtcactaagagcctt 710

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_hic.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_est7.*
- 9: gb_gsa1.*
- 10: gb_gsa2.*
- 11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708.4	99.8	725	8	CX752219
2	708.4	99.8	919	2	BG696407
3	708.4	99.8	1348	4	AF077198
4	704.4	99.2	1042	3	BM558765
5	701	98.7	1061	3	BM475259
6	700.4	98.6	2476	4	CR858568
7	690.8	97.3	904	7	CN805809
8	690.6	97.3	774	1	AU133073
9	679.4	95.7	711	3	BI550895
10	677.6	95.4	1088	3	BM465006
11	674.8	95.0	895	2	BG614082
12	673.2	94.8	889	3	BQ227373
13	670.4	94.4	691	3	BI906551
14	661.4	93.2	796	1	AU132495
15	660.4	93.0	896	2	BG528464
16	659.8	92.9	709	2	BG501911
17	656.4	92.5	1050	2	BG166847
18	655.2	92.3	798	7	CF994968
19	650	91.5	803	5	BX366646
20	648.4	91.3	898	2	BG613559
21	641.8	90.4	729	2	BG615693
22	640	90.1	765	2	BG722409

23	634	89.3	740	2	BG773497	BG773497
24	633.8	89.3	698	2	BG282835	BG282835
25	633.2	89.2	786	6	CB991804	CB991804
26	630	88.7	796	2	BE618034	BE618034
27	630	88.7	1161	3	BM457120	BM457120
28	629.8	88.7	838	1	AV757844	AV757844
29	625.8	88.1	815	8	CX754949	CX754949
30	614.4	86.5	895	2	BF314398	BF314398
31	613	86.3	658	6	CD701760	CD701760
32	609.4	85.8	705	7	CR750918	CR750918
33	609.4	85.8	931	2	BF970655	BF970655
34	605.8	85.3	853	3	BI549474	BI549474
35	605.6	85.3	725	3	BI596291	BI596291
36	602.4	84.8	1300	4	AF077199	AF077199
37	592.4	83.4	640	2	BG545991	BG545991
38	591.2	83.3	825	2	BG721347	BG721347
39	590	83.1	777	7	CO738296	CO738296
40	585.8	82.5	613	2	BG389590	BG389590
41	585.8	82.5	734	2	BG433925	BG433925
42	585.2	82.4	728	7	CO561951	CO561951
43	584	82.3	821	5	BQ440078	BQ440078
44	583.2	82.1	739	7	CN408025	CN408025
45	580.4	81.7	926	5	BQ899917	BQ899917

ALIGNMENTS

RESULT 1
CX752219
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

CX752219 725 bp mRNA linear EST 24-JAN-2005
AGENCOURT_40989196 NIH_MGC_281 Homo sapiens CDNA clone
IMAGE:7783359 3', mRNA sequence.
CX752219
CX752219.1 GI:58048874
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 725)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Meri Firpo
CDNA Library Preparation: Express Genomics
CDNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLAM15943 row: h column: 13
High quality sequence stop: 723.
Location/Qualifiers
i. .725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7783359"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 281"
/note="Organ: Blastocyst; Vector: pExpress-1; Site 1:
EcoRV; Site 2: NotI; RNA obtained from pluripotent_cell
line derived from blastocyst inner cell mass (cell line
HSF-6, NIH Registry designation UC06. Positive for OCT4

expression by rtPCR, positive for SSEA-3, SSEA-4, Tra-1-81, Tra-1-60 by immunofluorescence. Negative for SSEA-1 by immunofluorescence Passage 62. cDNA was primed using oligo-dT primer:
5'-pCAGTCTAGTCTAGTGGAGCGCGGCC('T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size selection >1.25 kb resulted in an average insert size of 2.0 kb. This primary library is normalized (non-normalized primary library is NIH-MGC 280) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

Query Match 99.8%; Score 708.4; DB 8; Length 725;
Best Local Similarity 99.9%; Pred. No. 3e-203; Mismatches 0; Indels 0; Gaps 0;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGGCGCAATAACATGTCACACCCCGCTGCCCGGCATCGTCCCGCGCGCGCGAAGGCC 60
DB 8 ATGTGGCGCAATAACATGTCACACCCCGCTGCCCGGCATCGTCCCGCGCGCGCGAAGGCC 67

QY 61 ACCGCTGCGGTGATTTCTCGATGGAATTGGAGATACATGGCAGCGATGGCAGAGCC 120
DB 68 ACCGCTGCGGTGATTTCTCGATGGAATTGGAGATACATGGCAGCGATGGCAGAGCC 127

QY 121 TTTGAGGTATCAGAGTTCACATATCAATATATCTGCCCATCGCGCTGTAGGCCT 180
DB 128 TTTGAGGTATCAGAGTTCACATATCAATATATCTGCCCATCGCGCTGTAGGCCT 187

QY 181 GTTACATTAATATGAACGTGGCTATGCCCTCATGTTTGTATTTATTTGGGCTTTACCA 240
DB 188 GTTACATTAATATGAACGTGGCTATGCCCTCATGTTTGTATTTATTTGGGCTTTACCA 247

QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGACGACAGAAATATAAAGCTTTGAT 300
DB 248 GATTCACAGGAGATGAATCTGGGATTAACAGGACGACAGAAATATAAAGCTTTGAT 307

QY 301 GATCAGAGTCAAGATGGCAATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 360
DB 308 GATCAGAGTCAAGATGGCAATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 367

QY 361 GGAGGAGCTTTATCTTTTATATCTGCCCTTACACACAGCAAGAACTGGCAGGTGCT 420
DB 368 GGAGGAGCTTTATCTTTTATATCTGCCCTTACACACAGCAAGAACTGGCAGGTGCT 427

QY 421 GCACCTAGTGTGGCTTCCACTTGGGCTTCCCTTTCCACAGGGTCTTATCGGTGGTCT 480
DB 428 GCACCTAGTGTGGCTTCCACTTGGGCTTCCCTTTCCACAGGGTCTTATCGGTGGTCT 487

QY 481 AATAGAGATTTCTTATCTCCAGTCCACGGGATTTGACCCCTTGGTCCCTGATG 540
DB 488 AATAGAGATTTCTTATCTCCAGTCCACGGGATTTGACCCCTTGGTCCCTGATG 547

QY 541 TTTGGTCTCTTACGGTGAAAAAATATAAACAATTTGGTGAATCCAGCAATGTGACCTTT 600
DB 548 TTTGGTCTCTTACGGTGAAAAAATATAAACAATTTGGTGAATCCAGCAATGTGACCTTT 607

QY 601 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGTCAGCAA 660
DB 608 AAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGATGTCAGCAA 667

QY 661 TTTCAATGATAAATCTTACCTCCATTTGATTCAGCTCACTAAGAGCCCTT 710
DB 668 TTTCAATGATAAATCTTACCTCCATTTGATTCAGCTCACTAAGAGCCCTT 717

RESULT 2
BG696407
LOCUS 919 bp mRNA linear EST 07-MAY-2001
DEFINITION 602659503F1 NCI_CGAP_skn3 Homo sapiens cDNA clone IMAGE:4802665 5', mRNA sequence.
ACCESSION BG696407
VERSION BG696407.1 GI:13961520

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

Sequencing by: Incyte Genomics, Inc.

Cloned through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10697 row: e column: 02

High quality sequence stop: 807.

Location/Qualifiers

1..919

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4802665"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

Technologies. Note: this is a NCI_CGAP Library."

Technologies. Note: this is a NCI_CGAP Library."

Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

0;

0;

0;

0;

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QY 481 AATAGAGATATTCTTATCTCCAGTGCACCGGGATGTGTGACCCCTTTGGTTCCTCCCTGATG 540
|||||
Db 497 AATAGAGATATTCTTATCTCCAGTGCACCGGGATGTGTGACCCCTTTGGTTCCTCCCTGATG 556
|||||
QY 541 TTTGGTCTCTTACCGTGAAAAAATCTAAACATTTGGTGAATCCAGCCATGTGACCTTT 600
|||||
Db 557 TTTGGTCTCTTACCGTGAAAAAATCTAAACATTTGGTGAATCCAGCCATGTGACCTTT 616
|||||
QY 601 AAAAAGCTATGAAGGTATGATGACAGTTCGTGTCAACAGCAAAATGATGATGTCAAGCAA 660
|||||
Db 617 ANAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGCAAAATGATGATGTCAAGCAA 676
|||||
QY 661 TTTCATTGATAAACTCTACCTCCAAATGATTCAGCTCACTAAGAGGCTTT 710
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Db 677 TTTCATTGATAAACTCTACCTCCAAATGATTCAGCTCACTAAGAGGCTTT 726
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RESULT 6
LOCUS CR858568 2476 bp mRNA linear HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA; cdna DKFZp45900134 (from clone DKFZp45900134).
ACCESSION CR858568
VERSION CR858568.1 GI:55728082
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.
REFERENCE 1 (bases 1 to 2476)
AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Wewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
CONSRMT The German CDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project. This clone (DKFZp45900134) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/ci.cgi?CloneID=DKFZp45900134
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
source

1..2476
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp45900134"
/tissue_type="cortex"
/clone_lib="459 (synonym: pcor1). Vector pSport1_Sfi; host
DH10B; sites SfiIa + SfiIb"
/dev_stage="adult"
/notes="lysophospholipase I (Homo sapiens)"
1..2476
/gene="DKFZp45900134"
76..768
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/codon_start=1
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/db_xref="GI:55728083"
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RSHIKYICPHAPVPTVLTNNMAMPWFEDIIIGLSPDSOEDSGIKQAAENIKALIDQ
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NRDISIQLCHGDGCDPLVPLMFGSLTVEKLTIVNPANVTFTKYEGBMHSSCCQEMMDV
KQFIDKLLPPIID"

gene

CDS

ORIGIN

Query Match 98.6%; Score 700.4; DB 4; Length 2476;
Best Local Similarity 99.2%; Pred. No. 1.2e-200;
Matches 704; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGTCGGCAATAACATGTCAACCGCTGCCCGCATCTGTCGCCCGCCCGCGAAGGCC 60
|||||
Db 76 ATGTCGGCAATAACATGTCAACCGCTGCCCGCATCTGTCGCCCGCCCGCGAAGGCC 135
|||||
QY 61 ACCGCTCGGGTGATTTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGCAGAAGCC 120
|||||
Db 136 ACCGCTCGGGTGATTTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGCAGAAGCC 195
|||||
QY 121 TTTGAGGTATCAGAAAGTTTCAATATATATCTGCCCGCATCTGTCGCCCGCTTTAGGCCT 180
|||||
Db 196 TTTGAGGTATCAGAAAGTTTCAATATATATCTGCCCGCATCTGTCGCCCGCTTTAGGCCT 255
|||||
QY 181 GTTACATTAAATATGCAAGTGTGCTATGCTTCATGTTTGATTTATTTATTTGGGCTTTTCACCA 240
|||||
Db 256 GTTACATTAAATATGCAAGTGTGCTATGCTTCATGTTTGATTTATTTGGGCTTTTCACCA 315
|||||
QY 241 GATTTCACAGGAGGATGAATCTGGGATTAAACAGGAGCAGAGAAAATATAAAAGCTTTGATT 300
|||||
Db 316 GATTTCACAGGAGGATGAATCTGGGATTAAACAGGAGCAGAGAAAATATAAAAGCTTTGATT 375
|||||
QY 301 GATCAAGAGTGAAGATGGCATTTCTTCTTAACAGAAATTTTGGGAGGGTTTCTCAG 360
|||||
Db 376 GATCAAGAGTGAAGATGGCATTTCTTCTTAACAGAAATTTTGGGAGGGTTTCTCAG 435
|||||
QY 361 GGAGAGCTTTTATCTTTATATATCTGCTTACACAGCAGCAAACTGTCAGGTGTCCT 420
|||||
Db 436 GGAGAGCTTTTATCTTTATATATCTGCTTACACAGCAGCAAACTGTCAGGTGTCCT 495
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QY 421 GCACCTCAGTGTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTATTCGGTGTGCT 480
|||||
Db 496 GCACCTCAGTGTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTATTCGGTGTGCT 555
|||||
QY 481 AATAGAGATATTCTTATCTCCAGTGCACCGGGATGTGTGACCCCTTTGGTTCCTCCCTGATG 540
|||||
Db 556 AATAGAGATATTCTTATCTCCAGTGCACCGGGATGTGTGACCCCTTTAGTTCCTCCCTGATG 615
|||||
QY 541 TTTGGTCTCTTACCGTGAAAAAATCTAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 600
|||||
Db 616 TTTGGTCTCTTACCGTGAAAAAATCTAAACATTTGGTGAATCCAGCCAAATGTGACCTTT 675
|||||
QY 601 AAAAAGCTATGAAGGTATGATGACAGTTCGTGTCAACAGCAAAATGATGATGTCAAGCAA 660
|||||
Db 676 AAAAAGCTATGAAGGTATGATGACAGTTCGTGTCAACAGCAAAATGATGATGTCAAGCAA 735
|||||
QY 661 TTTCATTGATAAACTCTACCTCCAAATGATTCAGCTCACTAAGAGGCTTT 710
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Db 736 TTTCATTGATAAACTCTACCTCCAAATGATTCAGCTCACTAAGAGGCTTT 785
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RESULT 7

CN805809

LOCUS

DEFINITION

5' similar to Bases 1 to 814 highly similar to human LYPLA1
(H8.446676), mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.

REFERENCE

AUTHORS

1 (bases 1 to 904)
Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agui,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.

TITLE

Analysis of the Macaca mulatta transcriptome and the sequence

JOURNAL
PUBMED
COMMENT

divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
15998449
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.12.06. 738 Q20 bases.
PCR Primers
FORWARD: CCTCACTAAGGGAACAAA
BACKWARD: CACTATAGGCGAATGGGTA
Insert Length: 904 Std Error: 0.00
Plate: CL000044 row: A column: 10
Seq primer: CCTCACTAAGGGAACAAA
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..904
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUV:14245"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="katze_MBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN

Query Match 97.3%; Score 690.8; DB 7; Length 904;
Best Local Similarity 98.3%; Pred. No. 7.1e-198;
Matches 698; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGTGGGCAATAACATGTCACACCGCGTCCCGCCATCGTCCCGCGCGCGCGGAGGCC 60
DB 5 ATGTGGGCAATAACATGTCACACCGCGTCCCGCCATCGTCCCGCGCGCGGAGGCC 64

QY 61 ACCGCTCGCGTATTTCTGATGATGGAGATCTGGGACGCGATGGGCGAGAGCC 120
DB 65 ACCGCTCGCGTATTTCTGATGATGGAGATCTGGGACGCGATGGGCGAGAGCC 124

QY 121 TTTCAGGATCAGAGTTCACATATCAATATATCTGCCGATCGCGCTGTAGGCCT 180
DB 125 TTTCAGGATCAGAGTTCACATATCAATATATCTGCCGATCGCGCTGTAGGCCT 184

QY 181 GTTACATTAATATGAACGTGCTATGCCTTCATGGTTGATATTTGGGCTTTTACCA 240
DB 185 GTTACATTAATATGAACGTGCTATGCCTTCATGGTTGATATTTGGGCTTTTACCA 244

QY 241 GATTCACAGGAGTGAATCTGGGATTAACAGGACGACAGAAATATAAAGCTTTGATT 300
DB 245 GATTCACAGGAGTGAATCTGGGATTAACAGGACGACAGAAATATAAAGCTTTGATT 304

QY 301 GATCAAGAGTGAAGATGGCATCTCTCTAACAGAAATATTTGGAGGGTTTCTCAG 360
DB 305 GATCAAGAGTGAAGATGGCATCTCTCTAACAGAAATATTTGGAGGGTTTCTCAG 364

QY 361 GGAGGAGCTTTATCTTTATATCTGCTTACACAGACAGAACTGGCAGTGTCACT 420
DB 365 GGAGGAGCTTTATCTTTATATCTGCTTACACAGACAGAACTGGCAGTGTCACT 424

QY 421 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGTCT 480
DB 425 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGTCCTATCGGTGTCT 484

QY 481 AATAGAGATATTTCTATCTCCAGTCCACAGGAGATTGACCCCTTGGTTCCCTGATG 540
DB 485 AATAGAGATATTTCTATCTCCAGTCCACAGGAGATTGACCCCTTGGTTCCCTGATG 544

QY 541 TTTGGTTCTCTTACGGTGGAAAAAATAAAAAATTGGTGAATCCAGCCAATGTGACCTTT 600
DB 545 TTTGGTTCTCTTACGGTGGAAAAAATAAAAAATTGGTGAATCCAGTCAATGTGACCTTT 604

QY 601 AAAACCTATGAAGGTATGATGACAGTTCGTGTCACAGGAAATGATGATGTCAGCNA 660
DB 605 AAAACCTATGAAGGTATGATGACAGTTCGTGTCACAGGAAATGATGATGTCAGCAA 664

QY 661 TTCATTGATAAATCCTACCTCCATTCATTGATGACCTCACTAAGAGGCCTT 710
DB 665 TTCATTGATAAATCCTACCTCCATTCATTGATGACCTCACTAAGAGGCCTT 714

RESULT 8
AUI33073

LOCUS
DEFINITION
AUI33073 NT2RP4 Homo sapiens cDNA clone NT2RP4001208 5', mRNA
sequence.

ACCESSION
AUI33073VERSION
AUI33073.1 GI:10993612KEYWORDS
EST.SOURCE
Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 774)

AUTHORS
Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Saito, K., Yamamoto, J.,
Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Masuho, Y., and
Isogai, T.

TITLE
HRI human cDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y.,
Saito, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T.,
Sugano, S., Masuho, Y., Isogai, T.)

JOURNAL

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

COMMENT
HRI human cDNA project; 5' - & 3' - end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

source

Location/Qualifiers
1..774
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP4001208"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RP4"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 97.3%; Score 690.6; DB 1; Length 774;
Best Local Similarity 99.2%; Pred. No. 7.8e-198;
Matches 704; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 ATGTGGGCAATAACATGTCACACCGCGTCCCGCCATCGTCCCGCGCGCGGAGGCC 60
DB 36 ATGTGGGCAATAACATGTCACACCGCGTCCCGCCATCGTCCCGCGCGGAGGCC 95

QY 61 ACCGCTCGCGTATTTCTGATGATGGAGATCTGGGACGCGATGGGCGAGAGCC 120
DB 96 ACCGCTCGCGTATTTCTGATGATGGAGATCTGGGACGCGATGGGCGAGAGCC 155

QY 121 TTTCAGGATCAGAGTTCACATATCAATATATCTGCCGATCGCGCTGTAGGCCT 180

156 TTTGAGGATATCAGAAATTCATATCAATATCAATATATCTGCCCGATGCGCTCTTAGGGCT 215
181 GTTACATTAATTAATGAACGTGCTATGCTTTCATGTTTGTATATATTTGGGCTTTTCAACA 240
216 GTTACATTAATTAATGAACGTGCTATGCTTTCATGTTTGTATATATTTGGGCTTTTCAACA 275
241 GATTACAGGAGGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAGCTTTGATT 300
276 GATTACAGGAGGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAGCTTTGATT 335
301 GATCAAGAGTCAAGATGGCAATCTCTTCAACAGAAATATTTTGGAGGGTTTCTCAG 360
336 GATCAAGAGTCAAGATGGCAATCTCTTCAACAGAAATATTTTGGAGGGTTTCTCAG 395
361 GGAGGAGCTTTATCTTTATATATCTGCTTACACACAGCAGAGAAATGTCAGGTGTCAC 420
396 GGAGGAGCTTTATCTTTATATATCTGCTTACACACAGCAGAGAAATGTCAGGTGTCAC 455
421 GCACCTAGTGTGGCTTCCACTTGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTGT 480
456 GCACCTAGTGTGGCTTCCACTTGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTGT 515
481 AATAGAGATATTTCTATTTCTCAGTCCACGGGGATTTGACCCCTTTGGTCCCTGTATG 540
516 AATAGAGATATTTCTATTTCTCAGTCCACGGGGATTTGACCCCTTTGGTCCCTGTATG 575
541 TTTGGTCTCTTACGGTGAAGAACTTAAACAACTTGGTGAATCCAGCCAAATGTGACCTTT 600
576 TTTGGTCTCTTACGGTGAAGAACTTAAACAACTTGGTGAATCCAGCCAAATGTGACCTTT 635
601 AAAACCTATGAAGGTATGATGCAC -AGTTCTGTCAACAGGAAATGATGGATGTCAAGCA 659
636 AAAACCTATGAAGGTATGATGCACAAAGTTCTGTCAACAGGAAATGATGGATGTCAAGCA 695
660 ATTCAITGATAAATCTTACCTCCATTCATTCAGCTCACTAAGAGGCTT 709
696 ATTCAITGATAAATCTTACCTCCATTCATTCAGCTCACTAAGAGGCTT 745

RESULT 9
B1550895
LOCUS 603195310F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5274938 5',
DEFINITION mRNA sequence.
ACCESSION B1550895
VERSION B1550895.1 GI:15438207
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 711)
NIH-MGC http://imgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11694 row: C column: 03
High quality sequence stop: 708.
Location/Qualifiers
1. .711
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source

/clone="IMAGE:5274938"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.5 kb and normalized to R0F 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN

Query Match 95.7%; Score 679.4; DB 3; Length 711;
Best Local Similarity 99.9%; Pred. No. 1.9e-194;
Matches 680; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGCGGCAATAACATGTCAACCCGCTGCCCGCATGTCGCCGCCCGCGGAGGCC 60
Db 31 ATGTGCGGCAATAACATGTCAACCCGCTGCCCGCATGTCGCCGCCCGCGGAGGCC 90
QY 61 ACCGCTGCGGTGATTTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGCAGAGCC 120
Db 91 ACCGCTGCGGTGATTTTCTGTCATGGATTGGGAGATCTGGGCACGGATGGCAGAGCC 150
QY 121 TTTGAGGATATCAGAAATTCACATATCAATATATCTGCCCGCATGCGCTGTAGGCT 180
Db 151 TTTGAGGATATCAGAAATTCACATATCAATATATCTGCCCGCATGCGCTGTAGGCT 210
QY 181 GTTACATTAATAATGAACGTGGCTTATGCTTTCATGTTTGTATATTTGGGCTTTTCAACA 240
Db 211 GTTACATTAATAATGAACGTGGCTTATGCTTTCATGTTTGTATATTTGGGCTTTTCAACA 270
QY 241 GATTACAGGAGGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAGCTTTGATT 300
Db 271 GATTACAGGAGGATGAATCTGGGATTAACAGGAGCAGAGAAATATAAAGCTTTGATT 330
QY 301 GATCAAGAGTCAAGAAATGGCATTCCTTCTAACAAGATTTATTTTGGAGGGTTTCTCAG 360
Db 331 GATCAAGAGTCAAGAAATGGCATTCCTTCTAACAAGATTTATTTTGGAGGGTTTCTCAG 390
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAGAAATGTCAGGTGTCAC 420
Db 391 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAGAAATGTCAGGTGTCAC 450
QY 421 GCACCTAGTGTGGCTTCCACTTGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTGT 480
Db 451 GCACCTAGTGTGGCTTCCACTTGGGCTTCCCTTCCACAGGGTCCCTATCGGTGGTGT 510
QY 481 AATAGAGATATTTCTATTTCTCAGTCCACGGGGATTTGTGACCTTTGGTTCCTCTGATG 540
Db 511 AATAGAGATATTTCTATTTCTCAGTCCACGGGGATTTGTGACCTTTGGTTCCTCTGATG 570
QY 541 TTTGGTCTCTTACCGTGGAAAACTTAAACAACTTGGTGAATCCAGCCAAATGTGACCTTT 600
Db 571 TTTGGTCTCTTACCGTGGAAAACTTAAACAACTTGGTGAATCCAGCCAAATGTGACCTTT 630
QY 601 AAAACCTATGAAGGTATGATGCACAGTTCGTGTCAACAGGAAATGATGATGTCAAGCA 660
Db 631 AAAACCTATGAAGGTATGATGCACAGTTCGTGTCAACAGGAAATGATGATGTCAAGCA 690
QY 661 TTCATTGATAAATCTCTACCT 681
Db 691 TTCATTGATAAATCTCTACCT 711

RESULT 10
B1550895
LOCUS 603195310F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5274938 5',
DEFINITION mRNA sequence.


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Matches 701; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
QY 1 ATGTGCGGCAATAACATGTCACACCGCGTCCCGCCGATCGTCCCGCGCGCGCGGAGGCC 60
Db 40 ATGTGCGGCAATAACATGTCACACCGCGTCCCGCCGATCGTCCCGCGCGCGGAGGCC 99
QY 61 ACCGCTGCGGCGATTTCTGTCGATGGATTTGGAGATATCTGGGACGAGATGGGACAGGCC 120
Db 100 ACCGCTGCGGCGATTTCTGTCGATGGATTTGGAGATATCTGGGACGAGATGGGACAGGCC 159
QY 121 TTTCAGAGTATCAGAAGTTCATATCAATATCAATATCTGCGCGATCTGGGCGTCTTAGGCT 180
Db 160 TTTCAGAGTATCAGAAGTTCATATCAATATCAATATCTGCGCGATCTGGGCGTCTTAGGCT 219
QY 181 GTTACATTAAATATGAACGTGCTATGCTTCAATGTTGATATATTTGGGCTTTTCACCA 240
Db 220 GTTACATTAAATATGAACGTGCTATGCTTCAATGTTGATATATTTGGGCTTTTCACCA 279
QY 241 GATTCCAGGAGATGAATCTGGGATTTAAACAGGACGAGAGAAATATAAAGCTTTGATT 300
Db 280 GATTCCAGGAGATGAATCTGGGATTTAAACAGGACGAGAGAAATATAAAGCTTTGATT 339
QY 301 GATCAAGAGTCAAGAGTGGCATCTCTTAACAGAGATTTTGGAGGTTTCTCAG 360
Db 340 GATCAAGAGTCAAGAGTGGCATCTCTTAACAGAGATTTTGGAGGTTTCTCAG 399
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAGAACTGGCAGGTGTCAT 420
Db 400 GGAGGAGCTTTATCTTTATATATCTGCTTACACAGCAGAGAACTGGCAGGTGTCAT 459
QY 421 GCACCTCAGTTGCTGCTTCCACTTCCGCGCTTCCCTTCCACAGGCTCTTATCGGTGCT 480
Db 460 GCACCTCAGTTGCTGCTTCCACTTCCGCGCTTCCCTTCCACAGGCTCTTATCGGTGCT 519
QY 481 AATAGAGATATTTCTATCTCAGTCCGCGGATTTGACCTTTGGTCCCTCGATG 540
Db 520 AATAGAGATATTTCTATCTCAGTCCGCGGATTTGACCTTTGGTCCCTCGATG 579
QY 541 TTGGTTCTCTTACGCGTGAAGAACTAAAAACATTCGTGAATCCAGCCTATGACCTTT 600
Db 580 TTGGTTCTCTTACGCGTGAAGAACTAAAAACATTCGTGAATCCAGCCTATGACCTTT 639
QY 601 AAAACCTATGAAGTATGATGACAGTTCTGTCGTCACAGGAAATGATGATGTCAGCAA 660
Db 640 AAAACCTATGAAGTATGATGACAGTTCTGTCGTCACAGGAAATGATGATGTCAGCAA 698
QY 661 TTCAATGTATAA-ACTCCTACCTCCAAATGATGATGACGTCACTAAGAGCCT 709
Db 699 TTCAATGTATAA-CTCCTACCTCCAAATGATGATGACGTCACTAAGAGCCT 748
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RESULT 12
BQ227373
LOCUS BQ227373
DEFINITION AGENCOURT_7566147 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6043585
5', mRNA sequence.
ACCESSION BQ227373
VERSION BQ227373.1 GI:20408773
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-x@mail.nih.gov
Tissue Procurement: AFCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13284 row: n column: 02
High quality sequence stop: 560.

FEATURES
source

Location/Qualifiers
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/mol_type="mRNA"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 94.8%; Score 673.2; DB 3; Length 889;
Best Local Similarity 98.5%; Pred. No. 1.6e-192;
Matches 700; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
QY 1 ATGTGCGGCAATAACATGTCACACCGCGTCCCGCCGATCGTCCCGCGCGCGGAGGCC 60
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QY 61 ACCGCTGCGGCGATTTCTGTCGATGGATTTGGAGATATCTGGGACGAGATGGGACAGGCC 120
Db 64 ACCGCTGCGGCGATTTCTGTCGATGGATTTGGAGATATCTGGGACGAGATGGGACAGGCC 122
QY 121 TTTCAGAGTATCAGAAGTTCATATCAATATATCTGCGCGATCGTCCCGCGCGCGGAGGCC 180
Db 123 TTTCAGAGTATCAGAAGTTCATATCAATATATCTGCGCGATCGTCCCGCGCGGAGGCC 182
QY 181 GTTACATTAAATATGAACGTGCTATGCTTCAATGTTGATATATTTGGGCTTTTCACCA 240
Db 183 GTTACATTAAATATGAACGTGCTATGCTTCAATGTTGATATATTTGGGCTTTTCACCA 242
QY 241 GATTCCAGGAGATGAATCTGGGATTTAAACAGGACGAGAGAAATATAAAGCTTTGATT 300
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QY 301 GATCAAGAGTCAAGAAATGGCAATTCCTTCTAACAAGATTTATTTGGAGGGTTTCTCAG 360
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QY 361 GGAGGAGCTTTATCTTTATATATCTGCGCTTACCAACAGCAGAGAACTGGCAGGTGTCAC 420
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QY 421 GCACCTCAGTTGCTGCTTCCACTTCCGCGCTTCCCTTCCACAGGCTCTTATCGGTGCT 480
Db 423 GCACCTCAGTTGCTGCTTCCACTTCCGCGCTTCCCTTCCACAGGCTCTTATCGGTGCT 482
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Db 483 AATAGAGATATTTCTATCTCAGTCCGCGGATTTGACCTTTGGTTCCTCCTGATG 542
QY 541 TTTCAGGTTCTTACGCGTGAAGAACTAAAAACATTCGTGAATCCAGCCTATGACCTTT 600
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QY 601 AAAACCTATGAAGTATGATGACAGTTCTGTCGTCACAGGAAATGATGATGTCAGCAA 660
Db 603 AAAACCTATGAAGTATGATGACAGTTCTGTCGTCACAGGAAATGATGATGTCAGCAA 662
QY 661 TTCAATGTATAA-CTCCTACCTCCAA-TTGATGACGTCACTAAGAGCCTT 710
Db 663 TTCAATGTATAA-CTCCTACCTCCAA-TTGATGACGTCACTAAGAGCCTT 713


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RESULT 13
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LOCUS      691 bp      mRNA      linear      EST 16-OCT-2001
DEFINITION 603064126F1 NTH_MGC_118 Homo sapiens cDNA clone IMAGE:5213143 5',
            mRNA sequence.
ACCESSION  BI906551
VERSION    BI906551.1 GI:16169292
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE  1 (bases 1 to 691)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LAM11535 row: d column: 08
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                /note="Vector: PCMV-SF0RT6; Site_1: NotI; Site_2: EcoRV
                (destroyed); RNA source leukocytes from anonymous pool of
                non-activated adult donors. Library is oligo-dr primed
                and directionally cloned (EcoRV site is destroyed upon
                cloning). Average insert size 1.7 kb, insert size range
                1.2-3.3 kb. Library is normalized and enriched for
                full-length clones and was constructed by C. Gruber
                (Invitrogen). Research Genetics tracking code 027. Note:
                this is a NIH_MGC Library."

ORIGIN
Query Match      94.4%; Score 670.4; DB 3; Length 691;
Best Local Similarity 99.7%; Pred. No. 1e-191;
Matches 682; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      1  ATGTGGCGCAATAACATGTCAACCCCGCTGCCCGCCATCGTCCCGCCCGCGGAAGGCC 60
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QY     61  ACCGCTCGCGTGATTTCTCGCATGATTTGGAGATACCTGGGCACGCGATGGGCAGAGCC 120
DB     68  ACCGCTCGCGTGATTTCTCGCATGATTTGGAGATACCTGGGCACGCGATGGGCAGAGCC 127

QY    121  TTTCAGGGTATCAGAAGTTACATATCAATATATCTGCCCGCATCGCTGTAGGCCT 180
DB    128  TTTCAGGGTATCAGAAGTTACATATCAATATATCTGCCCGCATCGCTGTAGGCCT 187

QY    181  GTTACATTAATAATGAACCGTGGTATCGCTTCATGTTTGGATTAATTGGGCTTTTCA 240
DB    188  GTTACATTAATAATGAACCGTGGTATCGCTTCATGTTTGGATTAATTGGGCTTTTCA 247

QY    241  GATTCCAGGAGGATGAATCTGGGATTAACAGGCAGCAGAAATATAAAGCTTTGATT 300
DB    248  GATTCCAGGAGGATGAATCTGGGATTAACAGGCAGCAGAAATATAAAGCTTTGATT 307
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QY      301  GATCAAGAAGTGAGAATGGCAATCCTTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 360
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QY     361  GGAGAGCTTTATCTTTTATATCTGCTTACCACACAGCAGAAACTGGCAGGTGTCACT 420
DB     368  GGAGAGCTTTATCTTTTATATCTGCTTACCACACAGCAGAAACTGGCAGGTGTCACT 427

QY     421  GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGT 480
DB     428  GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGT 487

QY     481  AATAGAGATATTTCTATTTCTCCAGTGCACACGGGGATTGTGACCCCTTTGGTTCCTCCCTGATG 540
DB     488  AATAGAGATATTTCTATTTCTCCAGTGCACACGGGGATTGTGACCCCTTTGGTTCCTCCCTGATG 547

QY     541  TTTGTTCTCTTACCGTGGAAAAAATAAAACATTGGTGAATCCAGCCAAATGTGACCTTT 600
DB     548  TTTGTTCTCTTACCGTGGAAAAAATAAAACATTGGTGAATCCAGCCAAATGTGACCTTT 607

QY     601  AAAACCTATGAGGTATGATGCACAGTTCGTCTCAACAGGAAATGATGATGTCAAGCAA 660
DB     608  AAAACCTATGAGGTATGATGCACAGTTCGTCTCAACAGGAAATGATGATGTCAAGCAA 667

QY     661  TTCATTGATAAACTCCTACCTCCA 684
DB     668  TTCATTGATAAACTCCTACCTCCA 691

RESULT 14
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DEFINITION AUI32495 NT2RP3 Homo sapiens cDNA clone NT2RP3004603 5', mRNA
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ACCESSION  AUI32495
VERSION    AUI32495.1 GI:10992849
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE  1 (bases 1 to 796)
            Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
            Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
            Isogai, T.
            HRI human cDNA project
            Unpublished (2000)
            Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
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ORIGIN
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Query Match	93.2%;	Score 661.4;	DB 1;	Length 796;
Best Local Similarity	97.9%;	Pred. No. 5.8e-189;		
Matches	699;	Conservative	0;	Mismatches 11; Indels 4; Gaps 3;
QY	1	ATGTGGCGCAATTAACATGTCACACCGCGCTGCCCGCATCGTGCCTGCCCGCGCGGAGGCC	60	
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QY	61	ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGCACGATGGGCGAGAAGCC	120	
DB	139	ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGCACGATGGGCGAGAAGCC	198	
QY	121	TTTGCAGGTATCAGAAAGTTCAATATCAATATATCTGCCCGCATCGGCTGTAGGCTT	180	
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QY	181	GTTACATTAATATGATGAACGCTGATGCTTCAATGCTTGTATTTGATATTTGGGCTTTCACCA	240	
DB	259	GTTACATTAATATGATGAACGCTGATGCTTCAATGCTTGTATTTGATATTTGGGCTTTCACCA	318	
QY	241	GATTCACAGAGATCAATCTGGGATTAACAGCGACGAGAAATATAAAGCTTTGATT	300	
DB	319	GATTCACAGAGATCAATCTGGGATTAACAGCGACGAGAAATATAAAGCTTTGATT	378	
QY	301	GATCAAGAGATGAAGATGGCAATTCCTTCTAACAGAAATATTTTGGAGGTTTCTCAG	360	
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DB	439	GGAGGAGCTTATCTTTATATATCTGCTTACACAGCAGAGAACTGGCAGTGTCAC	498	
QY	421	GCACCTCAGTTGCTGCTTCCACATTCGGGCTTCCCTTCCACAGGCTCTATCGGTGCT	480	
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QY	481	AATAGAGATATTTCTATTTCTCCAGTCCACGGGATTTGACCTTTGGTTCCTCCGTATG	540	
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DB	619	TTTGGTCTCTACCGTGGAACCTAAACACATTTGGTGAATCCAGCAATGTGACCTTT	678	
QY	601	AAACCTCTAGAGTATGATGCAC-AGTTCTGCTCAAC-AGGAAATGATGGATGTCAGC	658	
DB	679	AAACCTCTAGAGTATGATGCACAGTGTGATGATGATGATGATGATGATGATGATGATG	738	
QY	659	AATTCATTGATAAATCTCTACC--TCCAAATGATGACGTCACCTAAGAGGCTTT	710	
DB	739	AATTCATTGATAAATCTCTACCCTCCAAATGATGATGATGATGATGATGATGATGATG	792	
RESULT 15				
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LOCUS	602579913F1 NIH_MGC_60	Homo sapiens	cdna	clone IMAGE:4719051 5',
DEFINITION	mRNA sequence.			
ACCESSION	BG528464			
VERSION	BG528464.1	GI:13520001		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Hominidae; Homo.			
REFERENCE	N1H-MGC	http://mgi.nci.nih.gov/		
AUTHORS	(bases 1 to 896)			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-x@mail.nih.gov Tissue Procurement: DCTD/DTP			

cdna Library Preparation: CLONETECH Laboratories, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1571 row: i column: 04
High quality sequence stop: 697.
Location/Qualifiers
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/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATTTAGGCC-3' and 3' adaptor sequence: 5'-ATTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match	93.0%;	Score 660.4;	DB 2;	Length 896;
Best Local Similarity	97.5%;	Pred. No. 1.2e-188;		
Matches	692;	Conservative	0;	Mismatches 16; Indels 2; Gaps 2;
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DB	17	ATGTGGCGCAATTAACATGTCACACCGCGCTGCCCGCATCGTGCCTGCCCGCGCGGAGGCC	76	
QY	61	ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGCACGATGGGCGAGAAGCC	120	
DB	77	ACCGCTGCGGTGATTTCTCGCATGATTTGGGAGATCTGGGCACGATGGGCGAGAAGCC	136	
QY	121	TTTGCAGGTATCAGAAAGTTCAATATCAATATATCTGCCCGCATCGGCTGTAGGCTT	180	
DB	137	TTTGCAGGTATCAGAAAGTTCAATATCAATATATCTGCCCGCATCGGCTGTAGGCTT	196	
QY	181	GTTACATTAATATGAACGCTGATGCTTCAATGATTTGATATTTGGGCTTTCACCA	240	
DB	197	GTTACATTAATATGAACGCTGATGCTTCAATGATTTGATATTTGGGCTTTCACCA	256	
QY	241	GATTCACAGAGATGAATCTGGGATTAACAGCGACGAGAAATATAAAGCTTTGATT	300	
DB	257	GATTCACAGAGATGAATCTGGGATTAACAGCGACGAGAAATATAAAGCTTTGATT	316	
QY	301	GATCAAGAGATGAAGATGGCAATTCCTTCTAACAGAAATATTTTGGAGGTTTCTCAG	360	
DB	317	GATCAAGAGATGAAGATGGCAATTCCTTCTAACAGAAATATTTTGGAGGTTTCTCAG	376	
QY	361	GGAGGAGCTTATCTTTATATCTGCTTACACAGCAGAGAACTGGCAGGTGTCAC	420	
DB	377	GGAGGAGCTTATCTTTATATCTGCTTACACAGCAGAGAACTGGCAGGTGTCAC	436	
QY	421	GCACCTCAGTTGCTGCTTCCACATTCGGGCTTCCCTTCCACAGGCTCTATCGGTGCT	480	
DB	437	GCACCTCAGTTGCTGCTTCCACATTCGGGCTTCCCTTCCACAGGCTCTATCGGTGCT	496	
QY	481	AATAGAGATATTTCTATTTCTCCAGTCCACGGGATTTGACCTTTGGTTCCTCCGTATG	540	
DB	497	AATAGAGATATTTCTATTTCTCCAGTCCACGGGATTTGACCTTTGGTTCCTCCGTATG	556	
QY	541	TTTGGTCTCTTACCGTGGAACCTAAACACATTTGATGATCCAGCAATGTGACCTTT	600	

Db	557	-TTGGTTCTCTTACGGTGGAAAACT-AAAACATTGGTGAATCCAGCCAAATGTGACCTTT	614
Qy	601	AAAACTATGAAGGTATGATGCACAGTTTCGTGTCAACAGGAATGATGGATGTCAAGCAA	660
Db	615	AAAACTATGAAGGTATGATGCACAGTTTCGTGTCAACAGGAATGATGGATGTCAAGGCA	674
Qy	661	TTCAATTGATAAACTCCTACCTCCAATTGATTGACGTCACTAAAGAGCCTT	710
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:39:47 ; Search time 821 Seconds
(without alignments)
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Perfect score: 710
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Gapop 10.0 , Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708.4	99.8	1486	7	US-10-236-417-63 Sequence 63, Appl
2	708.4	99.8	1556	9	US-10-756-149-3671 Sequence 3671, Ap
3	708.4	99.8	2417	3	US-09-813-358-221 Sequence 221, App
4	708.4	99.8	2417	3	US-09-997-279-221 Sequence 221, App
5	708.4	99.8	2417	7	US-10-647-426-14 Sequence 14, Appl
6	708.4	99.8	2493	3	US-09-925-299-218 Sequence 218, App
7	708.4	99.8	2493	3	US-09-925-299-218 Sequence 218, App
8	708.4	99.8	2600	8	US-10-357-930-25196 Sequence 25196, A
9	686.4	96.7	1538	9	US-10-450-763-7268 Sequence 7268, Ap
10	668.4	94.1	701	7	US-10-210-130-55 Sequence 55, Appl
11	668.4	94.1	701	7	US-10-236-417-59 Sequence 59, Appl
12	604.4	85.1	2417	5	US-10-237-271-19 Sequence 19, Appl
13	566.4	79.8	2408	6	US-10-131-487A-156 Sequence 156, App
14	565	79.6	2396	5	US-10-106-698-1516 Sequence 1516, Ap
15	552.8	77.9	709	3	US-09-988-982-2 Sequence 2, Appli
16	495.2	69.7	521	8	US-10-696-639-1549 Sequence 1549, Ap
17	489.8	69.0	624	4	US-09-925-065A-624562 Sequence 624562, Sequence 624563
18	489.8	69.0	624	4	US-09-925-065A-624563 Sequence 624563, Sequence 624564
19	489.8	69.0	624	4	US-09-925-065A-624564 Sequence 624564, Sequence 624561
20	488.2	68.8	624	4	US-09-925-065A-624561 Sequence 61, Appl
21	408.8	57.6	616	7	US-10-236-417-61 Sequence 1369, Ap
22	404.4	57.0	416	3	US-09-878-178-1369 Sequence 1369, Ap
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C	24	404.4	57.0	416	5	US-10-146-502-1369	Sequence 1369, Ap
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	26	343.4	48.4	441	3	US-09-960-352-3924	Sequence 3924, Ap
	27	277.6	39.1	1624	6	US-10-359-499-15	Sequence 15, Appl
	28	277.6	39.1	1648	9	US-10-956-157-1750	Sequence 1750, Ap
	29	175.8	24.8	3673778	6	US-10-312-841-2	Sequence 2, Appli
	30	172.4	24.3	559	6	US-10-359-499-49	Sequence 49, Appl
	31	157.2	22.1	363	9	US-10-779-543-9796	Sequence 9796, Ap
	32	146.6	20.6	270	9	US-10-450-763-7267	Sequence 7267, Ap
	33	139.4	19.6	423	3	US-09-918-995-34606	Sequence 34606, A
	34	136.6	19.2	1208	10	US-11-097-143-28814	Sequence 28814, A
	35	135	19.0	782	3	US-09-813-358-220	Sequence 220, App
	36	135	19.0	782	3	US-09-997-279-220	Sequence 220, App
	37	128.8	18.1	461	3	US-09-813-358-207	Sequence 207, App
	38	128.8	18.1	461	3	US-09-997-279-207	Sequence 207, App
	39	123.6	17.4	3673778	6	US-10-312-841-1	Sequence 1, Appli
	40	104.4	14.7	106	3	US-09-998-598-2083	Sequence 2083, Ap
	41	100.2	14.1	3917	10	US-11-097-143-28813	Sequence 28813, A
	42	78.6	11.1	105	3	US-09-796-692-5977	Sequence 5977, Ap
	43	78.6	11.1	105	5	US-10-040-862-5977	Sequence 5977, Ap
	44	78.6	11.1	105	6	US-10-057-475B-5977	Sequence 5977, Ap
	45	78.6	11.1	105	6	US-10-154-884B-5977	Sequence 5977, Ap

ALIGNMENTS

RESULT 1
US-10-236-417-63
; Sequence 63, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 63
; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(766)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1308)...(1308)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1363)...(1363)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1365)...(1365)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1422)...(1422)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1424)...(1424)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
US-10-236-417-63

Query Match 99.8%; Score 708.4; DB 7; Length 1486;
Best Local Similarity 99.9%; Pred. No. 9.1e-211;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCGCGCGCGGGAAGGCC 60
DB 76 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCGCGCGCGGGAAGGCC 135
QY 61 ACCGCTGCGGTGATTTCTCGATCGGATTTGGGAGATCTGGGCACGGATGGCAGAAGCC 120
DB 136 ACCGCTGCGGTGATTTCTCGATCGGATTTGGGAGATCTGGGCACGGATGGCAGAAGCC 195
QY 121 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCGCTGTTAGGCTT 180
DB 196 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCGCTGTTAGGCTT 255
QY 181 GTTACATTAATAATGAACGTGCTATGCCCTCATGGTTTGATATTTGGGCTTTTCAACA 240
DB 256 GTTACATTAATAATGAACGTGCTATGCCCTCATGGTTTGATATTTGGGCTTTTCAACA 315
QY 241 GATTCACAGGAGTGAATCTGGGATTTAAACAGGACAGAGAAAATATAAAAGCTTTGATT 300
DB 316 GATTCACAGGAGTGAATCTGGGATTTAAACAGGACAGAGAAAATATAAAAGCTTTGATT 375
QY 301 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATTTTGGGAGGGTTTCTCAG 360
DB 376 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATTTTGGGAGGGTTTCTCAG 435
QY 361 GGAGGAGCTTTATCTTTATATCTGCTTATCTGCTTACACAGCAAACTGGCAGGTGTCAC 420
DB 436 GGAGGAGCTTTATCTTTATATCTGCTTATCTGCTTACACAGCAAACTGGCAGGTGTCAC 495
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGCTCCTATCGGTGGTCT 480
DB 496 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGCTCCTATCGGTGGTCT 555
QY 481 AATAGAGATATTTCTATTTCTCCAGTGCCACGGGGATTTGACCTTTTGGTTCCCTCGATG 540
DB 556 AATAGAGATATTTCTATTTCTCCAGTGCCACGGGGATTTGACCTTTTGGTTCCCTCGATG 615
QY 541 TTTCGTTCTTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCAATGTGACCTTTT 600
DB 616 TTTCGTTCTTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCAATGTGACCTTTT 675
QY 601 AAAACCTATGAAGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 660
DB 676 AAAACCTATGAAGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 735
QY 661 TTTCATGTAAACTCCTACCTCCAAATTTGATTTGACGTCACTTAAGAGCCCTT 710
DB 736 TTTCATGTAAACTCCTACCTCCAAATTTGATTTGACGTCACTTAAGAGCCCTT 785

RESULT 2
US-10-756-149-3671
; Sequence 3671, Application US/10756149
; Publication No. US20050181375A1

; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3671
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-3671

Query Match 99.8%; Score 708.4; DB 9; Length 1556;
Best Local Similarity 99.9%; Pred. No. 9.4e-211;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCGCGCGCGGGAAGGCC 60
DB 195 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCATCGTCCCGCGCGCGCGGGAAGGCC 254
QY 61 ACCGCTGCGGTGATTTCTCGATCGGATTTGGGAGATCTGGGCACGGATGGCAGAAGCC 120
DB 255 ACCGCTGCGGTGATTTCTCGATCGGATTTGGGAGATCTGGGCACGGATGGCAGAAGCC 314
QY 121 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCGCTGTTAGGCTT 180
DB 315 TTTCAGGATATCAGAAGTTTCAATATCAATATATCTGCCCGCATCGCGCTGTTAGGCTT 374
QY 181 GTTACATTAATAATGAACGTGCTATGCCCTCATGGTTTGATATTTGGGCTTTTCAACA 240
DB 375 GTTACATTAATAATGAACGTGCTATGCCCTCATGGTTTGATATTTGGGCTTTTCAACA 434
QY 241 GATTCACAGGAGTGAATCTGGGATTTAAACAGGACAGAGAAAATATAAAAGCTTTGATT 300
DB 435 GATTCACAGGAGTGAATCTGGGATTTAAACAGGACAGAGAAAATATAAAAGCTTTGATT 494
QY 301 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATTTTGGGAGGGTTTCTCAG 360
DB 495 GATCAAGAGTGAAGATGGCATTCCTTCTAAACAGAAATTTTGGGAGGGTTTCTCAG 554
QY 361 GGAGGAGCTTTATCTTTATATCTGCTTATCTGCTTACACAGCAAACTGGCAGGTGTCAC 420
DB 555 GGAGGAGCTTTATCTTTATATCTGCTTATCTGCTTACACAGCAAACTGGCAGGTGTCAC 614
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGCTCCTATCGGTGGTCT 480
DB 615 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCTTCCACAGGCTCCTATCGGTGGTCT 674
QY 481 AATAGAGATATTTCTATTTCTCCAGTGCCACGGGGATTTGACCTTTTGGTTCCCTCGATG 540
DB 675 AATAGAGATATTTCTATTTCTCCAGTGCCACGGGGATTTGACCTTTTGGTTCCCTCGATG 734
QY 541 TTTCGTTCTTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCAATGTGACCTTTT 600
DB 735 TTTCGTTCTTACGGTGAAAACTAAAAACATTTGGTGAATCCAGCAATGTGACCTTTT 794
QY 601 AAAACCTATGAAGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 660
DB 795 AAAACCTATGAAGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAA 854
QY 661 TTTCATGTAAACTCCTACCTCCAAATTTGATTTGACGTCACTTAAGAGCCCTT 710
DB 855 TTTCATGTAAACTCCTACCTCCAAATTTGATTTGACGTCACTTAAGAGCCCTT 904

RESULT 3
US-09-813-358-221
; Sequence 221, Application US/09813358
; Patent No. US20020048759A1

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Pyle, Ruth
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER
; FILE REFERENCE: 210121.501
; CURRENT APPLICATION NUMBER: US/09/813,358
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-358-221

Query Match 99.8%; Score 708.4; DB 3; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.2e-210;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAACATGTCACACCCCGCTGCCCGCATCGTCCGCGCCGCGGAGGCC 60
DB 36 ATGTGCGGCAATAACATGTCACACCCCGCTGCCCGCATCGTCCGCGCCGCGGAGGCC 95

QY 61 ACCGCTGCGGTGATTTCTGTCATGATTTGGAGATACCTGGGCACGGATGGGCAGAGCC 120
DB 96 ACCGCTGCGGTGATTTCTGTCATGATTTGGAGATACCTGGGCACGGATGGGCAGAGCC 155

QY 121 TTTCAGGATACAGAGTTTCAATATATATCTGCGCGCATCGTCCGCGCATGTTAGGCTT 180
DB 156 TTTCAGGATACAGAGTTTCAATATATATCTGCGCGCATCGTCCGCGCATGTTAGGCTT 215

QY 181 GTTACATTAATATGAACTGCTGCTTCAATATATCTGCGCGCATCGTCCGCGCATGTTAGGCTT 240
DB 216 GTTACATTAATATGAACTGCTGCTTCAATATATCTGCGCGCATCGTCCGCGCATGTTAGGCTT 275

QY 241 GATTCACAGGAGATGAATCTGGGATTTAAACAGGACAGAGAAATATAAAGCTTTGATT 300
DB 276 GATTCACAGGAGATGAATCTGGGATTTAAACAGGACAGAGAAATATAAAGCTTTGATT 335

QY 301 GATCAAGAGTGAAGATGGCATCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 360
DB 336 GATCAAGAGTGAAGATGGCATCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 395

QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTCAACAGAGAACTGGCAGGTGTCAC 420
DB 396 GGAGGAGCTTTATCTTTATATATCTGCTTCAACAGAGAACTGGCAGGTGTCAC 455

QY 421 GCACTCAGTTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGCT 480
DB 456 GCACTCAGTTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGCT 515

QY 481 AATAGAGATATTTCTATCTTCCAGTCCAGGGATTTGACCCCTTTGGTTCCCTGATG 540
DB 516 AATAGAGATATTTCTATCTTCCAGTCCAGGGATTTGACCCCTTTGGTTCCCTGATG 575

QY 541 TTTGGTTCTTACGGTGGAAAACTAAAAACATTTGGTGAATCCAGCAATGTGACCTTT 600
DB 576 TTTGGTTCTTACGGTGGAAAACTAAAAACATTTGGTGAATCCAGCAATGTGACCTTT 635

QY 601 AAAACCTATGAAGGTATGATGACAGTTCTGTCACAGGAAATGATGATGTCAGCA 660
DB 636 AAAACCTATGAAGGTATGATGACAGTTCTGTCACAGGAAATGATGATGTCAGCA 695

QY 661 TTCAATTGATAAACTCCCTACCTCAATTTGATTTGACGTCACTTAAGAGCCCTT 710
DB 696 TTCAATTGATAAACTCCCTACCTCAATTTGATTTGACGTCACTTAAGAGCCCTT 745

RESULT 4
US-09-997-279-221
; Sequence 221, Application US/09997279

; Publication No. US20030059781A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER
; FILE REFERENCE: 210121.501C1
; CURRENT APPLICATION NUMBER: US/09/997,279
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-279-221

Query Match 99.8%; Score 708.4; DB 3; Length 2417;
Best Local Similarity 99.9%; Pred. No. 1.2e-210;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAACATGTCACACCCCGCTGCCCGCATCGTCCGCGCCGCGGAGGCC 60
DB 36 ATGTGCGGCAATAACATGTCACACCCCGCTGCCCGCATCGTCCGCGCCGCGGAGGCC 95

QY 61 ACCGCTGCGGTGATTTCTGTCATGATTTGGAGATACCTGGGCACGGATGGGCAGAGCC 120
DB 96 ACCGCTGCGGTGATTTCTGTCATGATTTGGAGATACCTGGGCACGGATGGGCAGAGCC 155

QY 121 TTTCAGGATACAGAGTTTCAATATATATCTGCGCGCATCGTCCGCGCATGTTAGGCTT 180
DB 156 TTTCAGGATACAGAGTTTCAATATATATCTGCGCGCATCGTCCGCGCATGTTAGGCTT 215

QY 181 GTTACATTAATATGAACTGCTGCTTCAATATATCTGCGCGCATCGTCCGCGCATGTTAGGCTT 240
DB 216 GTTACATTAATATGAACTGCTGCTTCAATATATCTGCGCGCATCGTCCGCGCATGTTAGGCTT 275

QY 241 GATTCACAGGAGATGAATCTGGGATTTAAACAGGACAGAGAAATATAAAGCTTTGATT 300
DB 276 GATTCACAGGAGATGAATCTGGGATTTAAACAGGACAGAGAAATATAAAGCTTTGATT 335

QY 301 GATCAAGAGTGAAGATGGCATCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 360
DB 336 GATCAAGAGTGAAGATGGCATCTCTTAACAGAAATATTTTGGAGGGTTTCTCAG 395

QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTCAACAGAGAACTGGCAGGTGTCAC 420
DB 396 GGAGGAGCTTTATCTTTATATATCTGCTTCAACAGAGAACTGGCAGGTGTCAC 455

QY 421 GCACTCAGTTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGCT 480
DB 456 GCACTCAGTTGCTGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGCT 515

QY 481 AATAGAGATATTTCTATCTTCCAGTCCAGGGATTTGACCCCTTTGGTTCCCTGATG 540
DB 516 AATAGAGATATTTCTATCTTCCAGTCCAGGGATTTGACCCCTTTGGTTCCCTGATG 575

QY 541 TTTGGTTCTTACGGTGGAAAACTAAAAACATTTGGTGAATCCAGCAATGTGACCTTT 600
DB 576 TTTGGTTCTTACGGTGGAAAACTAAAAACATTTGGTGAATCCAGCAATGTGACCTTT 635

QY 601 AAAACCTATGAAGGTATGATGACAGTTCTGTCACAGGAAATGATGATGTCAGCA 660
DB 636 AAAACCTATGAAGGTATGATGACAGTTCTGTCACAGGAAATGATGATGTCAGCA 695

QY 661 TTCAATTGATAAACTCCCTACCTCAATTTGATTTGACGTCACTTAAGAGCCCTT 710
DB 696 TTCAATTGATAAACTCCCTACCTCAATTTGATTTGACGTCACTTAAGAGCCCTT 745

RESULT 5
US-10-647-426-14
; Sequence 14, Application US/10647426

Db 700 AAAACCTATGAAGGTATGATGACACAGTTCTGTCACACAGGAATGATGATGTCAGCAA 759
QY 661 TTCAATTGATAAACTCTTACTCTCAATTTGATTGACGTCACTAAGAGGCGCTT 710
Db 760 TTCAATTGATAAACTCTTACTCTCAATTTGATTGACGTCACTAAGAGGCGCTT 809

RESULT 7
US-09-925-299-218
; Sequence 218, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIORITY FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 218
; LENGTH: 2493
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-299-218

Query Match 99.8%; Score 708.4; DB 3; Length 2493;
Best Local Similarity 99.9%; Pred. No. 1.2e-210;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGATGTCACACCGCGCTGCGCCGATCGTCCGCGCGCGCGAGGCG 60
Db 100 ATGTGCGGCAATAAATGATGTCACACCGCGCTGCGCCGATCGTCCGCGCGCGCGAGGCG 159

QY 61 ACCGCTGCGGTGATTTCTGATGATGATGCGAGATCTGGGACGAGATGGGAGGCG 120
Db 160 ACCGCTGCGGTGATTTCTGATGATGATGCGAGATCTGGGACGAGATGGGAGGCG 219

QY 121 TTTCAGGATATCAGAGTTCACATATCAATATATCTGCGCGATCGGCTGTAGGCT 180
Db 220 TTTCAGGATATCAGAGTTCACATATCAATATATCTGCGCGATCGGCTGTAGGCT 279

QY 181 GTTACATTAATATGACGTGCTATGCTTCAATGTTGATATTTGATATTTGGCTTTTCCACCA 240
Db 280 GTTACATTAATATGACGTGCTATGCTTCAATGTTGATATTTGGCTTTTCCACCA 339

QY 241 GATTTCAGAGGATGAATCTGGGATTAACACGCGAGCAGAAATATAAAGCTTTGATT 300
Db 340 GATTTCAGAGGATGAATCTGGGATTAACACGCGAGCAGAAATATAAAGCTTTGATT 399

QY 301 GATCAAGAGTGAAGATGCGATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 360
Db 400 GATCAAGAGTGAAGATGCGATCTCTTCAACAGAAATATTTTGGAGGTTTCTCAG 459

QY 361 GGAGGAGCTTTATCTTTATATCTGCGCTTACACACAGCAGAAATCTGGCAGGTGTCAT 420
Db 460 GGAGGAGCTTTATCTTTATATCTGCGCTTACACACAGCAGAAATCTGGCAGGTGTCAT 519

QY 421 GCACCTAGTTGCTGGCTTCCACCTTCCGCTTCCCTTCCACAGGCTCTCTATCGGTGGTCT 480
Db 520 GCACCTAGTTGCTGGCTTCCACCTTCCGCTTCCCTTCCACAGGCTCTCTATCGGTGGTCT 579

QY 481 AATAGAGATATTTCTATTTCTTCCAGTGCACCGGAGATTTGACCTTTTGGTTCCCTGATG 540
Db 580 AATAGAGATATTTCTATTTCTTCCAGTGCACCGGAGATTTGACCTTTTGGTTCCCTGATG 639

QY 541 TTTCGTTCTCTTACGTTGGAAAAAATCTTAAACATTTGTTGATTCACGCAATGTGACCTTT 600
Db 640 TTTCGTTCTCTTACGTTGGAAAAAATCTTAAACATTTGTTGATTCACGCAATGTGACCTTT 699

QY 601 AAAACCTATGAAGGTATGATGACACAGTTCTGTCACACAGGAATGATGATGTCAGCAA 660
Db 700 AAAACCTATGAAGGTATGATGACACAGTTCTGTCACACAGGAATGATGATGTCAGCAA 759

QY 661 TTCAATTGATAAACTCTTACTCTCAATTTGATTGACGTCACTAAGAGGCGCTT 710
Db 760 TTCAATTGATAAACTCTTACTCTCAATTTGATTGACGTCACTAAGAGGCGCTT 809

RESULT 8
US-10-357-930-25196
; Sequence 25196, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIORITY FILING DATE: 2003-02-04
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25196
; LENGTH: 2600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1, 2600
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-25196

Query Match 99.8%; Score 708.4; DB 8; Length 2600;
Best Local Similarity 99.9%; Pred. No. 1.3e-210;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGCGGCAATAAATGATGTCACACCGCGCTGCGCCGATCGTCCGCGCGCGCGAGGCG 60
Db 163 ATGTGCGGCAATAAATGATGTCACACCGCGCTGCGCCGATCGTCCGCGCGCGCGAGGCG 222

QY 61 ACCGCTGCGGTGATTTCTGATGATGATGCGAGATCTGGGACGAGATGGGAGGCG 120
Db 223 ACCGCTGCGGTGATTTCTGATGATGATGCGAGATCTGGGACGAGATGGGAGGCG 282

QY 121 TTTCAGGATATCAGAGTTCACATATCAATATATCTGCGCGATCGGCTGTAGGCT 180
Db 283 TTTCAGGATATCAGAGTTCACATATCAATATATCTGCGCGATCGGCTGTAGGCT 342

QY 181 GTTACATTAATATGACGTGCTATGCTTCAATGTTGATATTTGGCTTTTCCACCA 240
Db 343 GTTACATTAATATGACGTGCTATGCTTCAATGTTGATATTTGGCTTTTCCACCA 402

QY 241 GATTTCAGAGGATGAATCTGGGATTAACACGCGAGCAGAAATATAAAGCTTTGATT 300
Db 403 GATTTCAGAGGATGAATCTGGGATTAACACGCGAGCAGAAATATAAAGCTTTGATT 462

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QY 301 GATCAAGAGTGAAGAAATGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTTCTCAG 360
Db |||||
463 GATCAAGAGTGAAGAAATGGCATTCCTCTTAACAGAAATATTTTGGAGGGTTTTCTCAG 522
QY 361 GGAGGAGCTTTATCTTTTATATATCTGCGCTTACACAGAGAAACTGGCAGGTGTCACT 420
Db |||||
523 GGAGGAGCTTTATCTTTTATATATCTGCGCTTACACAGAGAAACTGGCAGGTGTCACT 582
QY 421 GCACCTAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGTGGTGTCT 480
Db |||||
583 GCACCTAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGTGGTGTCT 642
QY 481 AATAGAGATATTTCTATTTCTCAGTGCACAGGGGATTTGACCCCTTTGGTTCCCTCGATG 540
Db |||||
643 AATAGAGATATTTCTATTTCTCAGTGCACAGGGGATTTGACCCCTTTGGTTCCCTCGATG 702
QY 541 TTTGGTTCTCTTACGGTGAAGAAACTTAAACAACTTGGTGAATCCAGCCCAATGTGACCTTT 600
Db |||||
703 TTTGGTTCTCTTACGGTGAAGAAACTTAAACAACTTGGTGAATCCAGCCCAATGTGACCTTT 762
QY 601 AAAACCTATGAAGGTATGATGACACAGTTCGTGTCAACAGGAATGATGGATGTCAAGCAA 660
Db |||||
763 AAAACCTATGAAGGTATGATGACACAGTTCGTGTCAACAGGAATGATGGATGTCAAGCAA 822
QY 661 TTTCAATTGATAAACTCTACCTCCAAATTGATTGACGTCACTAAGAGGCCTT 710
Db |||||
823 TTTCAATTGATAAACTCTACCTCCAAATTGATTGACGTCACTAAGAGGCCTT 872
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RESULT 9

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US-10-450-763-7268
; Sequence 7268, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 7268
; LENGTH: 1538
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-763-7268
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Query Match 96.7%; Score 686.4; DB 9; Length 1538;
Best Local Similarity 99.6%; Pred. No. 7.4e-204;
Matches 709; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 ATGTGGCGCAATAACATGTCAACCCCGTGCCTCCCGCCATCGTGCCTCCCGCCCGCGGAGGCC 60
Db |||||
195 ATGTGGCGCAATAACATGTCAACCCCGTGCCTCCCGCCATCGTGCCTCCCGCCCGCGGAGGCC 254
QY 61 ACCGCTGCGGTGATTTTCTCGATGATTTGGGAGATCTGGGACGCGATGGGCGAGAGCC 120
Db |||||
255 ACCGCTGCGGTGATTTTCTCGATGATTTGGGAGATCTGGGACGCGATGGGCGAGAGCC 314
QY 121 TTTGACGGTATCAGAAGTTTACATATCAATATATCTGCCCGCATCGCCTGTATTAGGCT 180
Db |||||
315 TTTGACGGTATCAGAAGTTTACATATCAATATATCTGCCCGCATCGCCTGTATTAGGCT 374
QY 181 GTTACATTAAATATGAACTGGCTATGCCTTCATGG-TTTGATATTTATTTGGGCTTTTACC 239
Db |||||
375 GTTACATTAAATATGAACTGGCTATGCCTTCATGGTTTGTATTTATTTGGGCTTTTACC 434
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QY 240 AGATTCACAGGAGGATGAATCTGGGATTAACACAGCAGAGAAAATATATAAAAGCTTTGAT 299
Db |||||
435 AGATTCACAGGAGGATGAATCTGGGATTAACACAGCAGAGAAAATATATAAAAGCTTTGAT 494
QY 300 TGATCAAGAGTGAAGAAATGGCAATTCCTCTTAACAGAAATATTTT-GGGAGGGTTTCTC 358
Db |||||
495 TGATCAAGAGTGAAGAAATGGCAATTCCTCTTAACAGAAATATTTTGGGGAGGGTTTCTC 554
QY 359 AGGAGGAGCTTTATCTTTTATATATCTGCCCTTACCACAGCAGAGAAAATCTGGCAGGTGTCA 418
Db |||||
555 AGGAGGAGCTTTATCTTTTATATATCTGCCCTTACCACAGCAGAGAAAATCTGGCAGGTGTCA 614
QY 419 CTGCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGTGGTGG 478
Db |||||
615 CTGCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGTGGTGG 674
QY 479 CTAATAGAGATATTTCTATTTCTCAGTGCACGGGATTTGACCCCTTTGGTTCCCTCTGA 538
Db |||||
675 CTAATAGAGATATTTCTATTTCTCAGTGCACGGGATTTGACCCCTTTGGTTCCCTCTGA 734
QY 539 TGTTTGGTTCTCTTACGGTGGAAAAAATAAAAAATTTGGTGAATCCAGCCAATGTGACCT 598
Db |||||
735 TGTTTGGTTCTCTTACGGTGGAAAAAATAAAAAATTTGGTGAATCCAGCCAATGTGACCT 794
QY 599 TTAAACCTATCAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGC 658
Db |||||
795 TTAAACCTATCAGGTATGATGACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGC 854
QY 659 AATTCATTGATAAACTCTTACCTCCAATTGATTGACGTCACTAAGAGGCCTT 710
Db |||||
855 AATTCATTGATAAACTCTTACCTCCAATTGATTGACGTCACTAAGAGGCCTT 906
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RESULT 10
US-10-210-130-55
; Sequence 55, Application US/10210130
; Publication No. US20040014053A1
; GENERAL INFORMATION:
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Patturajan, Meera
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Li, Li
; APPLICANT: Berghs, Constance
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Smithson, Glennda
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Leite, Mario W.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Anderson, David W.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Khrantsov, Nikolai V.
; APPLICANT: Ort, Tatiana
; APPLICANT: Ellerman, Karen
; APPLICANT: Rastelli, Luca
; APPLICANT: Agee, Michele L.
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Chant, John S.
; APPLICANT: DiPippo, Vincent A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Gangolli, Esha A.


```
APPLICANT: Giot, Ioic
APPLICANT: Ooi, Chean Eng
APPLICANT: Rothenberg, Mark E.
APPLICANT: Spaderma, Steven K.
APPLICANT: Hjalte, Tord
APPLICANT: Liu, Xiaohong
APPLICANT: Taupier, Raymond J., Jr.
APPLICANT: Catterton, Elina
APPLICANT: Shenoy, Suresh G.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-416C (Cura-716 SMT)
CURRENT APPLICATION NUMBER: US/10/210,130
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/316,508
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/354,655
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/383,887
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/323,936
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/381,039
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 369
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 55
LENGTH: 701
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (8)..(697)
US-10-210-130-55

Query Match          94.1%; Score 668.4; DB 7; Length 701;
Best Local Similarity 97.7%; Pred. No. 2.1e-198;
Matches 678; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCCATCGTGGCCCGCCGCGGGAAGGCC 60
Db 8 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCCATCGTGGCCCGCCGCGGGAAGGCC 67
QY 61 ACCGCTGCGGTGATTTTCTGCAATGATGGAGATCTGGGCACGCGATGGGCGAGAAGCC 120
Db 68 ACCACTGAGTGATTTTCTGCAATGATGGAGATCTGGGCACGCGATGGGCGAGAAGCC 127
QY 121 TTGCAAGTATCAGAGTTACATATCAATATATCTGCCCGCATCGCTGTTAGGCTT 180
Db 128 TTGCGCGGATCAATAGTTACATATCAATATATCTGCCCGCATCGCTGTTAGGCTT 187
QY 181 GTTACATTAATATGAACGGTGTATGCCCTTCATGGTTGATATTTGGCTTTTCACCA 240
Db 188 GTTACATTAATATGAACATAGTATGCCCTTCATGGTTGATATTTGGCTTTTCACCA 247
QY 241 GATTTCAGAGGATGAATCTGGGATTAACAGGACGAGAAATAATAAAGCTTTGATT 300
Db 248 GATTTCAGAGGATGAATCTGGGATTAACAGGACGAGCAAAATAATAAAGCTTTGATT 307
QY 301 GATCAAGAGTGAAGATGCGATTCCTTTCAACAGAAATATTTTGGAGGGTTTCTCAG 360
Db 308 GATCAAGAGTGAAGATGCGATTCCTTTCAACAGAAATATTTTGGAGGGTTTCTCAG 367

361 GGAGGAGCTTTATCTTTATATACTGCCCTTACCACACAGCAGAAACTGCGAGGTGTCACT 420
368 GGAGGAGCTTTATCTTTATATACTGCCCTTACCACACAGCAGAAACTGCGAGGTGTCACT 427
421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGTGCT 480
428 GCACCTCAATTTGCTGGCTTCCACTTTGGGCTTCTTTCCACAGGGTCTTATCGGTGTGCT 487
481 AATAGAGATATTTCTATTCTCCAGTGCACGGGGATTTGACCCCTTTGGTTCCCTGTGATG 540
488 AATAGAGATATTTCTATTCTCCAGTGCACGGGGATTTGACCCCTTTGGTTCCCTGTGATG 547
541 TTGTTCTCTTACGGTGGAAAACTAAACAACTTGGTAATCCAGCCAACTGTGACCTTTT 600
548 TTGTTCTCTTACGGTGGAAAACTAAACAACTTGGTAATCCAGCCAACTGTGACCTTTT 607
601 AAAACCTATGAGGTATGATGCACAGTTCGTGTCAACAGGAATGATGATGTCAAGCAA 660
608 AAAACCTATGAGGTATGATGCACAGTTCGTGTCAACAGGAATGATGATGTCAAGCAA 667
661 TTCAATTGATAAACTCCTACCTCCAATTGATTGAC 694
668 TTCAATTGATAAACTCCTACCTCCAATTGATTGAC 701

RESULT 11
US-10-236-417-59
; Sequence 59, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 59
; LENGTH: 701
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8)..(698)
; US-10-236-417-59

Query Match          94.1%; Score 668.4; DB 7; Length 701;
Best Local Similarity 97.7%; Pred. No. 2.1e-198;
Matches 678; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGTGGGCAATAACATGTCAACCCCGCTGCCCGCCATCGTGGCCCGCCGCGGGAAGGCC 60
```

Db 8 ATGTGCGCAATAAATCATGTCAACCCCGCTGCCCATCGTCCCGCCCGCCCGGAAGGCC 67
QY 61 ACCGTGCGGTGATTTCTGTCATGGATGGGAGATCTGGGCACGGATGGCAGAGCC 120
Db 68 ACCACTGAGGTGATTTCTGTCATGGATGGGAGATCTGGGCACGGATGGCAGAGCC 127
QY 121 TTTGCGAGGTATCAGAAAGTTCAATATCAATATATCTGCCCATCGCGCTGTTAGGCCT 180
Db 128 TTTGCGGTATCATAGTTCAATATCAATATATCTGCCCATCGCGCTGTTAGGCCT 187
QY 181 GTTACATTAATATGAACGTGCTATGCTTCAATGTTTGAATATTTAGGCTTTTCAACA 240
Db 188 GTTACATTAATATGAACATAGCTATGCTTCAATGTTTGAATATTTAGGCTTTTCAACA 247
QY 241 GATTCACAGGAGATGAATCTGGGATTAACAGGACGAGAGAAATATAAAGCTTTGATT 300
Db 248 GATTCACAGGAGATGAATCTGGGATTAACAGGACGAGCAAAATATAAAGCTTTGATT 307
QY 301 GATCAAGAAGTGAAGATGGCATTCCTTCTAACAGAAATATTTTGGGAGGTTTCTCAG 360
Db 308 GATCAAGAAGTGAAGATGGCAATCTCTCTAACAGAAATATTTTGGGAGGTTTCTCAG 367
QY 361 GGAGGAGCTTTATCTTTATATATCTGCTTACACACAGCAAACTGGCAGGTGTCACT 420
Db 368 GGAGGAGCTTTATCTTTATATATCTGCTTACACACAGCAAACTGGCAGGTGTCACT 427
QY 421 GCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGGTGCT 480
Db 428 GCACTCAATTTGCTGGCTTCCACTTTGGGCTTCCCTTCCACAGGTCCTATCGGTGCT 487
QY 481 AATAGAGATATTTCTATCTCAGTGCACGGGATTTGACCCCTTTGGTTCCCTCTGATG 540
Db 488 AATAGAGATATTTCTATCTCAGTGCACGGGATTTGACCCCTTTGGTTCCCTCTGATG 547
QY 541 TTTGGTTCTTTACGGTGGAAAACTAAAAAATTTGGTGAATCCAGCCAATGTGACCTTT 600
Db 548 TTTGGTTCTTTACGGTGGAAAACTAAAAAATTTGGTGAATCCAGCCAATGTGACCTTT 607
QY 601 AAAACCTATGAAGGTATGATGACAGTTGCTGTCAACAGGAATGATGATGTCAAGCA 660
Db 608 AAAACCTATGAAGGTATGATGACAGTTGCTGTCAACAGGAATGATGATGTCAAGCA 667
QY 661 TTCAATTGATAAACTCCTACCTCCAATTGATTGAC 694
Db 668 TTCAATTGATAAACTCCTACCTCCAATTGATTGAC 701

RESULT 12

US-10-237-271-19
; Sequence 19, Application US/10237271
; Publication No. US20030096328A1
; GENERAL INFORMATION:
; APPLICANT: THE BURNHAM INSTITUTE
; APPLICANT: SMITH, Jeffrey W.
; APPLICANT: KRIDEL, Steven J.
; APPLICANT: AXELROD, Fumiko T.
; TITLE OF INVENTION: SERINE/THREONINE HYDROLASE PROTEINS AND SCREENING ASSAYS
; FILE REFERENCE: BURN100-1
; CURRENT APPLICATION NUMBER: US/10/237,271
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 60/317,842
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(2417)
; OTHER INFORMATION: n is any nucleotide
US-10-237-271-19

RESULT 13

US-10-131-487A-156
; Sequence 156, Application US/10131487A
; Publication No. US20040009478A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TUMOR TISSUE
; FILE REFERENCE: ALBRE 11
; CURRENT APPLICATION NUMBER: US/10/131,487A
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/623,791A
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/DE99/00721
; PRIOR FILING DATE: 1999-03-09

Query Match 85.1%; Score 604.4; DB 5; Length 2417;
Best Local Similarity 86.7%; Pred. No. 5,1e-178;
Matches 617; Conservative 0; Mismatches 93; Indels 2; Gaps 1;
QY 1 ATGTGCGCAATAAATCATGTCAACCCCGTGGCCCATCGTGGCCCGCCCGCGAAGGCC 60
Db 36 ATGTGCGCAATAAATCATGTCAACCCCGTGGCCCATCGTGGCCCGCCCGCGAAGGCC 95
QY 61 ACCGTGCGGTGATTTCTGTCATGGATGGGAGATCTGGGCACGGATGGCAGAGCC 120
Db 96 ACCGTGCGGTGATTTCTGTCATGGATGGGAGATCTGGGCACGGATGGCAGAGCC 155
QY 121 TTTGCGAGGTATCAGAAAGTTCAATATCAATATATCTGCCCATCGCGCTGTTAGGCCT 180
Db 156 TTTGCGGTATCAGAAAGTTCAATATCAATATATCTGCCCATCGCGCTGTTAGGCCT 215
QY 181 GTT--ACATTAATAATGAACGTGGCTATGCTTCAATGTTTGAATATTTAGGCTTTTCA 238
Db 216 GTTNANCATTAATATGAACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 275
QY 239 CAGATTCACAGGAGATGAATCTGGGATTAACAGGACGACAGAAATATAAAGCTTTGA 298
Db 276 CAGATTCACAGGAGATGAATCTGGGATTAACAGGACGACAGAAATANNNNNNNNNN 335
QY 299 TTGATCAAGAAGTGAAGAATGGCATTCCTTCTAACAGAAATATTTTGGAGGGTTTCTC 358
Db 336 NNN 395
QY 359 AGGAGGAGCTTTATCTTTATATATCTGCCCTTACACACAGCAGAAACTGGCAGGTGA 418
Db 396 NNGGAGGAGCTTTATCTTTATATATCTGCCCTTACACACAGCAGAAACTGGCAGGTGA 455
QY 419 CTGCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGGTGG 478
Db 456 CTGCACTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGTCCTATCGGTGG 515
QY 479 CTAATAGAGATATTTCTATTTCTCCAGTGCACGGGATTTGTGACCTTTGGTTCCCTGA 538
Db 516 CTAATAGAGATATTTCTATTTCTCCAGTGCACGGGATTTGTGACCTTTGGTTCCCTGA 575
QY 539 TGTTTGGTTCTCTACGGTGGAAAACTAAAAAATTTGGTGAATCCAGCCAATGTGACCT 598
Db 576 TGTTTGGTTCTCTACGGTGGAAAACTAAAAAATTTGGTGAATCCAGCCAATGTGACCT 635
QY 599 TTAAAAACCTATGAAGGTATGATGACAGTTCTGTCTCAACAGGAAATGATGATGTCAAG 658
Db 636 TTAAAAACCTATGAAGGTATGATGACAGTTCTGTCTCAACAGGAAATGATGATGTCAAG 695
QY 659 AATTCATTGATAAACTCCTACCTCCAATTTGATTGACGTCACTAAGAGGCTTT 710
Db 696 AATTCATTGATAAACTCCTACCTCCAATTTGATTGACGTCACTAAGAGGCTTT 747

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; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 2408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-487A-156

Query Match      79.8%; Score 566.4; DB 6; Length 2408;
Best Local Similarity 90.6%; Pred. No. 4.2e-166;
Matches 643; Conservative 0; Mismatches 1; Indels 66; Gaps 1;

QY 1 ATGTGGGCAATAAATGATGCAACCGCGCTGCGCCGATCGTGCCTCCCGCCCGCGAAGGCC 60
DB 70 ATGTGGGCAATAAATGATGCAACCGCGCTGCGCCGATCGTGCCTCCCGCCCGCGAAGGCC 129
QY 61 ACCGCTGCGGTGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 130 ACCGCTGCGGTGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 170
QY 121 TTTCAGAGTATCAGAAAGTTTCAATATATATCTGCGCCGATCGTGCCTGTTAGGCCT 180
DB 171 -----GCTGTGTAGGCCT 183
QY 181 GTTACATTAAATATGAACGCTGCTATGCTTTCATGTTTGTATATATGCGCTTTTCCACCA 240
DB 184 GTTACATTAAATATGAACGCTGCTATGCTTTCATGTTTGTATATATGCGCTTTTCCACCA 243
QY 241 GATTACAGAGATGAATCTGGGATTAACAGGAGCAGAAATATAAAGCTTTTGATT 300
DB 244 GATTACAGAGATGAATCTGGGATTAACAGGAGCAGAAATATAAAGCTTTTGATT 303
QY 301 GATCAAGAGATGAAGAAATGCAATCTCTTCAAGAAATATTTTGGAGGCTTTTCTCAG 360
DB 304 GATCAAGAGATGAAGAAATGCAATCTCTTCAAGAAATATTTTGGAGGCTTTTCTCAG 363
QY 361 GGAGGAGCTTTATCTTTTATATATCTGCTTACACAGCAGAAATCGCAGGTGTCAT 420
DB 364 GGAGGAGCTTTATCTTTTATATATCTGCTTACACAGCAGAAATCGCAGGTGTCAT 423
QY 421 GCATCAGTTGCTGGCTTCCACTTCCGCTTCCCTTCCACAGGCTCCTATCGGTGCT 480
DB 424 GCATCAGTTGCTGGCTTCCACTTCCGCTTCCCTTCCACAGGCTCCTATCGGTGCT 483
QY 481 AATAGAGATATTTCTATTTCTCAGTCCAGCGGATTTGACCTTTTCCCTCTGATG 540
DB 484 AATAGAGATATTTCTATTTCTCAGTCCAGCGGATTTGACCTTTTCCCTCTGATG 543
QY 541 TTTGGTTCTCTTACGGTGGAAACTTAAACAAATTTGGTGAATCCAGCCAAATGTGACCTTT 600
DB 544 TTTGGTTCTCTTACGGTGGAAACTTAAACAAATTTGGTGAATCCAGCCAAATGTGACCTTT 603
QY 601 AAAACCTATGAAGTATGATGACAGTTGCTGTCACAGGAAATGATGATGTCAGCAA 660
DB 604 AAAACCTATGAAGTATGATGACAGTTGCTGTCACAGGAAATGATGATGTCAGCAA 663
QY 661 TTCAATTGATAAACTCTTACCTCAATTTGATGACGTCACCTAAGAGGCTTT 710
DB 664 TTCAATTGATAAACTCTTACCTCAATTTGATGACGTCACCTAAGAGGCTTT 713

RESULT 14
US-10-106-698-1516
; Sequence 1516, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
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; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1516
; LENGTH: 2396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1516

Query Match      79.6%; Score 565; DB 5; Length 2396;
Best Local Similarity 90.3%; Pred. No. 1.2e-165;
Matches 641; Conservative 1; Mismatches 2; Indels 66; Gaps 1;

QY 1 ATGTGGGCAATAAATGATGCAACCGCGCTGCGCCGATCGTGCCTCCCGCCCGCGAAGGCC 60
DB 36 ATGTGGGCAATAAATGATGCAACCGCGCTGCGCCGATCGTGCCTCCCGCCCGCGAAGGCC 95
QY 61 ACCGCTGCGGTGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 96 ACCGCTGCGGTGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
QY 121 TTTCAGAGTATCAGAAAGTTTCAATATATATCTGCGCCGATCGTGCCTGTTAGGCCT 180
DB 137 -----GCTGTGTAGGCCT 149
QY 181 GTTACATTAAATATGAACGCTGCTATGCTTTCATGTTTGTATATATGCGCTTTTCCACCA 240
DB 150 GTTACATTAAATATGAACGCTGCTATGCTTTCATGTTTGTATATATGCGCTTTTCCACCA 209
QY 241 GATTACAGAGATGAATCTGGGATTAACAGGAGCAGAAATATAAAGCTTTTGATT 300
DB 210 GATTACAGAGATGAATCTGGGATTAACAGGAGCAGAAATATAAAGCTTTTGATT 269
QY 301 GATCAAGAGATGAAGAAATGCGCATTCCTTCTAAGAAATATTTTGGAGGCTTTTCTCAG 360
DB 270 GATCAAGAGATGAAGAAATGCGCATTCCTTCTAAGAAATATTTTGGAGGCTTTTCTCAG 329
QY 361 GGAGGAGCTTTATCTTTTATATATCTGCTTACACAGCAGAAATCGCAGGTGTCAT 420
DB 330 GGAGGAGCTTTATCTTTTATATATCTGCTTACACAGCAGAAATCGCAGGTGTCAT 389
QY 421 GCACTCAGTTGCTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGCTCCTATCGGTGCT 480
DB 390 GCACTCAGTTGCTGGCTTCCACTTTCGGGCTTCCCTTCCACAGGCTCCTATCGGTGCT 449
QY 481 AATAGAGATATTTCTATTTCTCAGTCCAGCGGATTTGACCTTTTGGTTCCTCTGATG 540
DB 450 AATAGAGATATTTCTATTTCTCAGTCCAGCGGATTTGACCTTTTGGTTCCTCTGATG 509
QY 541 TTTGGTTCTCTTACGGTGGAAACTTAAACAAATTTGGTGAATCCAGCCAAATGTGACCTTT 600
DB 510 TTTGGTTCTCTTACGGTGGAAACTTAAACAAATTTGGTGAATCCAGCCAAATGTGACCTTT 569
QY 601 AAAACCTATGAAGTATGATGACAGTTGCTGTCACAGGAAATGATGATGTCAGCAA 660
DB 570 AAAACCTATGAAGTATGATGACAGTTGCTGTCACAGGAAATGATGATGTCAGCAA 629
QY 661 TTCAATTGATAAACTCTTACCTCAATTTGATGACGTCACCTAAGAGGCTTT 710
DB 630 TTCAATTGATAAACTCTTACCTCAATTTGATGACGTCACCTAAGAGGCTTT 679

RESULT 15
```

US-09-988-982-2
: Sequence 2, Application US/09988982
: Patent No. US20020081699A1
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: Shah, Purvi
: Murry, Lynn E.
: TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/988,982
: FILING DATE: 19-No. US20020081699A1-2001
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/213,394
: FILING DATE: <unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0269 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 709 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: KIDNNOT19
: CLONE: 2676650
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-988-982-2
Query Match 77.9%; Score 552.8; DB 3; Length 709;
Best Local Similarity 89.9%; Pred. No. 3.8e-162;
Matches 630; Conservative 1; Mismatches 4; Indels 66; Gaps 1;
QY 1 ATGTGGGCAATAACATGTCAACCCCGCTGCCGCCATCGTCCCGCCGCGCCGCGGAGGCC 60
Db |||||||
75 ATGTGGGCAATAACATGTCAACCCCGCTGCCGCCATCGTCCCGCCGCGCCGCGGAGGCC 134
QY 61 ACCGCTGCGGTGATTTCTCGATGGATTGGGAGATCTGGGCGACGGATGGGCGAGAGCC 120
Db |||||||
135 ACCGCTGCGGTGATTTCTCGATGGATTGGGAGATCTGG----- 175
QY 121 TTTCAGGATATCAGAGTTTACATATACAAATATATCTGCCCGCATGCGCCTGTAGGCCT 180
Db |||||||
176 -----GCCTGTTAGGCCT 188
QY 181 GTTACATTAATGAACTGGCTATGCCTTCATGTTTGATATATTGGGCTTTCACCA 240
Db |||||||
189 GTTACATTAATGAACTGGCTATGCCTTCATGTTTGATATATTGGGCTTTCACCA 248
QY 241 GATTACAGAGGATCAATCTGGGATTAAACAGGCGACAGAAAATAATAAAGCTTTGATT 300
Db |||||||
249 GATTACAGAGGATCAATCTGGGATTAAACAGGCGACAGAAAATAATAAAGCTTTGATT 308
QY 301 GATCAAGAGTGAAGATGGCATTCCTTTCTAACAGAAATTTATTTGGAGGGTTTCTCAG 360
Db |||||||
309 GATCAAGAGTGAAGATGGCATTCCTTTCTAACAGAAATTTATTTGGAGGGTTTCTCAG 368

QY 361 GGAGGAGCTTTATCTTTATATATACTCCCTTACCAACAGCAGAAACTGGCAGGTGTCACT 420
Db |||||||
369 GGAGGAGCTTTATCTTTATATATACTCCCTTACCAACAGCAGAAACTGGCAGGTGTCACT 428
QY 421 GCACCTCAGTTGCTGGCTTCCACTTCGGGCTTCCCTTCCACAGGGTCTTATCGGTGGTGT 480
Db |||||||
429 GCACCTCAGTTTCTTCTGCTTCCACTTCGGGNTTCTTTTCCACAGGRCCTATCGGTGGTGT 488
QY 481 AATAGAGATATTTCTATTCTCCAGTCCACGGGATTTGTAGCCCTTTGGTTCCCTCTGATG 540
Db |||||||
489 AATAGAGATATTTCTATTCTCCAGTCCACGGGATTTGTAGCCCTTTGGTTCCCTCTGATG 548
QY 541 TTTGGTTCTCTTACCGTGGAAAACTAAAAACAATTTGGTGAATCCAGCCCAATGTGACCTTT 600
Db |||||||
549 TTTGGTTCTCTTACCGTGGAAAACTAAAAACAATTTGGTGAATCCAGCCCAATGTGACCTTT 608
QY 601 AAAACCTATGAAGGTATGATGCACAGTTCTGTGTCAACAGGAAATGATGGATGTCAAGCAA 660
Db |||||||
609 AAAACCTATGAAGGTATGATGCACAGTTCTGTGTCAACAGGAAATGATGGATGTCAAGCAA 668
QY 661 TTCATTGATTAACCTCCTACCTCCAATTTGATTGACGCTCACTA 701
Db |||||||
669 TTCATTGATAAACTCCTACCTCCAATTTGATTGACGCTCACTA 709

Search completed: April 14, 2006, 16:02:12
Job time : 824 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 12:53:38 ; Search time 667 Seconds
(without alignments)
4287.496 Million cell updates/sec

Title: US-09-493-601B-1
Perfect score: 710
Sequence: 1 atgtgcggcaataacatgtc.....tgacgtcactaagagcctt 710

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New.*

- 1: /SIDSS/prodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /SIDSS/prodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS/prodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/prodata/2/pubpna/PCT_NEW_PUB.seq.*
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- 10: /SIDSS/prodata/2/pubpna/US10_NEW_PUB.seq.*
- 11: /SIDSS/prodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /SIDSS/prodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /SIDSS/prodata/2/pubpna/US11_NEW_PUB.seq.*
- 14: /SIDSS/prodata/2/pubpna/US11_NEW_PUB.seq.*
- 15: /SIDSS/prodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	489.8	69.0	624	6	US-09-925-065A-624562
C 2	489.8	69.0	624	6	US-09-925-065A-624563
C 3	489.8	69.0	624	6	US-09-925-065A-624564
C 4	488.2	68.8	624	6	US-09-925-065A-624561
5	282.4	39.8	1591	14	US-11-136-527-98
6	68.4	9.6	70	8	US-10-310-914A-5212
7	68.2	9.6	852	5	US-09-978-360A-38
8	63	8.9	86950	8	US-10-857-780-5
9	58	8.2	90	8	US-10-310-914A-5211
10	55	7.7	684	9	US-10-932-182A-3117
11	55	7.7	684	9	US-10-932-182A-3117
12	53.4	7.5	468	9	US-10-932-182A-82374
13	53.4	7.5	468	9	US-10-932-182A-82374
14	37.6	5.3	8098	8	US-10-995-561-255
15	37.6	5.3	10407	8	US-10-995-561-261
16	37.6	5.3	16792	8	US-10-995-561-262
17	37.6	5.3	17292	8	US-10-995-561-260
18	37.6	5.3	17436	8	US-10-995-561-257

19	37.6	5.3	17507	8	US-10-995-561-254	Sequence 254, App
20	37.6	5.3	17610	8	US-10-995-561-258	Sequence 258, App
21	37.6	5.3	17642	8	US-10-995-561-256	Sequence 256, App
22	37.6	5.3	19023	8	US-10-995-561-259	Sequence 259, App
23	36	5.1	816	6	US-09-925-065A-7143	Sequence 7143, App
24	36	5.1	816	9	US-10-301-480-108380	Sequence 108380, App
25	36	5.1	816	10	US-10-301-480-721789	Sequence 721789, App
C 26	35.6	5.0	569	6	US-09-925-065A-896666	Sequence 896666, App
27	35.6	5.0	592	6	US-09-925-065A-821995	Sequence 821995, App
C 28	35.6	5.0	935	10	US-10-301-480-556693	Sequence 556693, App
C 29	35.6	5.0	935	10	US-10-301-480-1170102	Sequence 1170102, App
C 30	35.6	5.0	989	10	US-10-301-480-556694	Sequence 556694, App
C 31	35.6	5.0	989	10	US-10-301-480-1170103	Sequence 1170103, App
C 32	35.6	5.0	662	9	US-10-301-480-56079	Sequence 56079, App
C 33	35.4	5.0	662	10	US-10-301-480-669488	Sequence 669488, App
34	35.4	5.0	180654	14	US-11-121-086-58	Sequence 58, App
35	35	4.9	1023	6	US-09-925-065A-90993	Sequence 90993, App
36	35	4.9	1023	9	US-10-301-480-192234	Sequence 192234, App
37	35	4.9	1023	10	US-10-301-480-805643	Sequence 805643, App
38	34.8	4.9	3635	6	US-09-925-065A-719292	Sequence 719292, App
39	34.8	4.9	3635	6	US-09-925-065A-719293	Sequence 719293, App
C 40	34.6	4.9	79122	14	US-11-117-187-200	Sequence 200, App
C 41	34.4	4.8	592	6	US-09-925-065A-749212	Sequence 749212, App
C 42	34.4	4.8	818	10	US-10-301-480-569297	Sequence 569297, App
C 43	34.4	4.8	818	10	US-10-301-480-1182706	Sequence 1182706, App
44	34	4.8	783	6	US-09-925-065A-29672	Sequence 29672, App
45	34	4.8	783	9	US-10-301-480-130910	Sequence 130910, App

ALIGNMENTS

RESULT 1
US-09-925-065A-624562/c
; Sequence 624562, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 624562
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-624562

Query Match	69.0%;	Score	489.8;	DB	6;	Length	624;
Best Local Similarity	97.1%;	Pred. No.	1.7e-134;				
Matches	508;	Conservative	1;	Mismatches	13;	Indels	1;
						Gaps	1;
QY	1	ATGTGGGCAATACATGTCACCCCGCTGCCCGCATCGTCCCGCCCGCGGAAGGCC	60				
DB	523	ATGTGGGCAATACATGTCACCCCGCTGCCCGCATCGTCCCGCCCGCGGAAGGCC	464				
QY	61	ACCGTCGCGTATTTCTCGATGATGGAGATCTGGGCACGGATGGGAGAGCC	120				
DB	463	ACCRCTGAGTGATTTCTCGATGATGGAGATCTGGGCACGGATGGGAGAGCC	404				

452	Qy	CCCTTCCACAGGCTCTATCGGTGGTGTCTAATAGAGATATTTCTATTCTCCAGTGCACG	511
548	Db	ACTTCCCCAAGCAGCCAAATGCGCATGCGCAAG--GACCTGGCCATCTTTCAATGCGCAG	604
512	Qy	GGGATGTGACCCCTTTGGTTCCTCGATGTTTGGTTCCTTACGGTGGAAAACTAAAA	571
605	Db	GGGAGTGGACCCCAATGGTACCTGTCGGTTTGGGGCCCTGACAGCTGAGAGCTCCGGA	664
572	Qy	CATTGGTGAATCCAGCCCAATGTGACCTTTTAAAACTATAGAGGTATGATGCACAGTTCGT	631
665	Db	CAGTTGTACACTGCCAGGGTCCAGTTTAAAGACATACCCAGGTGTGATGCACAGTCTCT	724
632	Qy	GTCAACAGGAAATGATGGATGTCAAGCAATTCATTGATAAATCCTACCTCC	683
725	Db	GTCTTCAGCAGATGTCAGCTGTAAAGGAATTTCTGGAGAACTTCTGCCTCC	776

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RESULT 6
US-10-310-914A-5212
; Sequence 5212, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5212
; LENGTH: 70
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-5212

Query Match          9.6%; Score 68.4; DB 8; Length 70;
Best Local Similarity 62.9%; Pred. No. 3.8e-10;
Matches 44; Conservative 25; Mismatches 1; Indels 0; Gaps 0;

Qy      310 GTGAAGAATGGCATTCCTTCTAAACAGAAATTATTTGGGAGGTGTTTTCTCAGGGAGGAGCT 369
        :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db       1   GUGAAGRAUUGGCCAUUUCCUCURACAGAAUAUUUGCGGAGGUUUUUUCUGCAGGAGAGCU 60

Qy      370 TTATCTTTAT 379
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Db       61 UUAUCUUUAV 70
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RESULT 7
US-09-978-360A-38
; Sequence 38, Application US/09978360A
; Publication No. US2006009633A9
; GENERAL INFORMATION: Jean-Baptiste Dumas Milne
; APPLICANT: Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56. US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116

/	PRIOR FILING DATE:	1998-08-10
/	PRIOR APPLICATION NUMBER:	US 60/099,273
/	PRIOR FILING DATE:	-09-04
/	PRIOR APPLICATION NUMBER:	US 09/191,997
/	PRIOR FILING DATE:	1998-11-13
/	PRIOR APPLICATION NUMBER:	US 09/215,435
/	PRIOR FILING DATE:	1998-12-17
/	PRIOR APPLICATION NUMBER:	PCT/IB98/02122
/	PRIOR FILING DATE:	1998-12-17
/	PRIOR APPLICATION NUMBER:	US 09/247,155
/	PRIOR FILING DATE:	1999-02-09
/	Remaining Prior Application data removed - See File Wrapper or PALM.	
/	NUMBER OF SEQ ID NOS:	810
/	SOFTWARE:	Patent.pm
/	SEQ ID NO	38
/	LENGTH:	852
/	TYPE:	DNA
/	ORGANISM:	Homo Sapiens
/	FEATURE:	
/	NAME/KEY:	CDS
/	LOCATION:	229..735
/	FEATURE:	
/	NAME/KEY:	sig peptide
/	LOCATION:	229..492
/	OTHER INFORMATION:	Von Heijne matrix
/	OTHER INFORMATION:	score 6.70
/	OTHER INFORMATION:	seq VFALSSFLNKASA/VY
/	FEATURE:	
/	NAME/KEY:	polyA signal
/	LOCATION:	816..821
/	FEATURE:	
/	NAME/KEY:	polyA site
/	LOCATION:	841..852
/	US-09-978-360A-38	

Query Match	9.6%	Score 68.2;	DB 5; Length 852;
Best Local Similarity	47.5%;	Pred. No. 1.5e-09;	Gaps 1
Matches 252; Conservative 0; Mismatches 263; Indels 16; Gaps 1			
Qy	18	GTCAACCCCGCTGCGGCCCATCGTGGCGCGCGCCGGAAGGCCACCCTGGCGTGATTTT	77
Db	41	GTGGTTCGCGGGCTGTATGTGTGGCGCAGGAGGCATAGCGGCTCTCTGATCTT	100
Qy	78	CCTGCATPGATTGGAGATACTGGCACGGATGGCGCAAGCCCTT-----	122
Db	101	CCTGCATGGCTCAGGTGATTCTGCACAAGGATTAAAGAATTGGATCAAGCAGGTTTTTA	160
Qy	123	TGCAGGTATCAGNAGTTCCATATCAAATATATCTCCCCCATCGCGCTGTTAGGCCTG	181
Db	161	ATCAAGATTTAACATTCCAACACATAAAAAATTATTC AACAGCTCCTCCAGATCAT	220
Qy	182	TTACATTAAATATGAACGTGGCTATGCTTCATGTTTGATATTATTCGGCTTTCCACCAG	241
Db	221	ATACTCTATGAAGGAGGATCTCCCAATGTATGGTTGACAGATTTAAAATAACCAATG	280
Qy	242	ATTCACAGGAGGATGAATCTGGGATTAAACAGGCAGCAGAAAAATATAAAGCTTTGATG	301
Db	281	ACTGCCAGAACACCTTTGAATCAATTGATGT CATGTGTCAAGTGCTTACTGATTTGATG	340
Qy	302	ATCAGAAGTGAAGATGGCANCTCTTCTTAACAGAAATATTTTGGGAGGTTTTTCTCAGG	361
Db	341	ATGAAGAAGTAAAAAGTGGCATCAAGAAGAACAGGATATTAAATAGGAGGATTTCTCTATGG	400
Qy	362	GAGGAGCTTTATCTTTATATACTGCCCTTACACACAGCAGAAACTGGCAGGTGTCACTG	421
Db	401	GAGGATGCATGGCAATGCATTTAGCATATAGAAATCATCAGATGTGCAGAGGATTTTG	460
Qy	422	CACTCAGTGTGGCTTTCCACTTCGGGCTCCCCTTCCACAGGGTCCCTATCGGTGGTGCTA	481
Db	461	CTCTTTCTAGTTTTCTGAATAAAGCATCTGCTGTGTTTACCAGGCTCTTCAGAAGAGTAATG	520
Qy	482	ATAGAGATATTTCTATTCTTCAGTGCACGGGGATTGTGACCTTTGGTTC	532

Db 319 GGCATTAAACCGGAACAGATCATCATTTGGGGGTTCTCTCAAGTGCTGCAATTTGGCCCTG 378
QY 379 TATACCTGCCCTTACACACAGAGAACTGGCAGGTGTCACTGCACCTCAGTTGCTGGCTT 438
Db 379 GCATCATCTGTCACTTTACCATGGAAGTGC CGGTATAGTCGCACATCCGGGTTTGGT 438
QY 439 CCACCTTCGGGCTTCCTCCACAGGTCCTATCGGTGGTGCTAAATAGAGATATTTCTATT 498
Db 439 TACATTCGGGAATCTTGAACA---ACACAAGACGATCTCAACGTCAAGACACCCATT 495
QY 499 CTCAGTGCACCGGGAATGTGACCCCTTTGGTTCCTCCCTGATGTTGGTTCCTTTACGGTG 558
Db 496 TTTACGGACATGGCGATATGATCCAGTTGTACCTATAGCACTTTGGCTTGAGCGCAAAA 555
QY 559 GAAAACTTAAACATTTGGTGAATCCAGCCCAATGTGACCTTTAAACACCTATGAAGGTATG 618
Db 556 AAATTTCTACCAAGACCTTGAACA---ACACAAGACGATCTCAACGTCAAGACACCCATT 495
QY 499 CTCAGTGCACCGGGAATGTGACCCCTTTGGTTCCTCCCTGATGTTGGTTCCTTTACGGTG 558
Db 496 TTTACGGACATGGCGATATGATCCAGTTGTACCTATAGCACTTTGGCTTGAGCGCAAAA 555
QY 559 GAAAACTTAAACATTTGGTGAATCCAGCCCAATGTGACCTTTAAACACCTATGAAGGTATG 618
Db 556 AAATTTCTACCAAGACCTTGAACA---ACACAAGACGATCTCAACGTCAAGACACCCATT 495
QY 619 ATGCACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAATTCATTGATAACTCTTA 678
Db 616 GCACATTTACAGTTCTCGAGGAACCTGGACGACTTAACCTGCCTTCTTTAAGAAATGCCTA 675
QY 679 CCT 681
Db 676 TCT 678

RESULT 11
US-10-932-182A-3117
; Sequence 3117, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3117
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3117

Query Match 7.7%; Score 55; DB 9; Length 684;
Best Local Similarity 46.4%; Pred. No. 1.1e-05;
Matches 252; Conservative 0; Mismatches 285; Indels 6; Gaps 2;
QY 142 CATATCAATATATCTGCCGCGATCGCCTGTAGGCTGTACATTAATATGAACGTG 201
Db 139 CACAAACCTTTGATATCCCAATGCTCCAGAGTCCATGTGACAGCAAAACGGTGTGCA 198
QY 202 GCTATGCCCTTCATGGTTTGATATTATG---GGCTTTCCACAGATTCACAGGAGGATGAA 258
Db 199 TTGATGCCCTGTGGTTTGACATCTAGAGTGGGATTCAGTTTTCACAAAGTTGATAGC 258
QY 259 TCTGGATTAACAGGACGACAGAAATATAAAGCTTTGATTCAGATTCACAGAGGATGAA 318
Db 259 GATGGATTCATGAATTCCTTAAATGCCATTGAAAAGACGGTTAAACAGGAAATGACAAG 318
QY 319 GGCATTTCTCTTAAACAGAAATATTTTGGAGGCTTTCTCAGGAGGAGCTTTATCTTTA 378
Db 319 GGCATTAACCGGAACAGATCATCATTTGGGGGTTCTCTCAGGTGCTGCAATTTGGCCCTG 378
QY 379 TATACCTGCCCTTACCAACAGAGAACTGGCAGGTGTCACTGCATCAGTTCTGGCTT 438
Db 379 GCATCATCTGTCACTTTTACCATGGAAGTCCGCGGTATAGTCGCACATCTCGGCTTTTGGT 438

QY 439 CCACCTTCGGGCTTCCTTCCACAGGTCCTATCGGTGGTGCTAAATAGAGATATTTCTATT 498
Db 439 TACATTCGGGAATCTTGAACA---ACACAAGACGATCTCAACGTCAAGACACCCATT 495
QY 499 CTCAGTGCACCGGGAATGTGACCCCTTTGGTTCCTCCCTGATGTTGGTTCCTTTACGGTG 558
Db 496 TTTACGGACATGGCGATATGATCCAGTTGTACCTATAGCACTTTGGCTTGAGCGCAAAA 555
QY 559 GAAAACTTAAACATTTGGTGAATCCAGCCCAATGTGACCTTTAAACACCTATGAAGGTATG 618
Db 556 AAATTTCTACCAAGACCTTGAACA---ACACAAGACGATCTCAACGTCAAGACACCCATT 495
QY 619 ATGCACAGTTCGTGTCAACAGGAAATGATGGATGTCAAGCAATTCATTGATAACTCTTA 678
Db 616 GCACATTTACAGTTCTCGAGGAACCTGGACGACTTAACCTGCCTTCTTTAAGAAATGCCTA 675
QY 679 CCT 681
Db 676 TCT 678

RESULT 12
US-10-932-182A-82374
; Sequence 82374, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82374
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-82374

Query Match 7.5%; Score 53.4; DB 9; Length 468;
Best Local Similarity 51.6%; Pred. No. 2.7e-05;
Matches 148; Conservative 0; Mismatches 136; Indels 3; Gaps 1;
QY 142 CATATCAATATATCTGCCGCGATCGCCTGTAGGCTGTACATTAATATGAACGTG 201
Db 139 CATACTAATTTTGTGTTTTCCTTAATGCTCCAGAGCTTCATGTGACAGCAAAACGGCGTGCA 198
QY 202 GCTATGCCCTTCATGGTTTGATATTATG---GGCTTTCCACAGATTCACAGGAGGATGAA 258
Db 199 TTGATGCCCTGTGGTTTGACATCTTGGAAATGGGATCCTAGTTTTCACAAAGTTGACAGT 258
QY 259 TCTGGATTAACAGGACGACGAGAAATATAAAGCTTTGATTCATCAAGAACTGAAGAAT 318
Db 259 GACGGTTTATGAATCTTTGAAATTCATAGAAAAGACGGTTAAGCAAGAAATGTATAA 318
QY 319 GGCATTTCTCTTAAACAGAAATATTTTGGAGGCTTTCTCAGGAGGAGCTTTATCTTTA 378
Db 319 GGAATTAACCGGAGCAGATTTATTCGAGGTTTCTCTCAGGTTGCCGCAATTAGCTCTC 378
QY 379 TATACCTGCCCTTACCAACAGAGAACTGGCAGGTGTCACTGCACCT 425
Db 379 GCAACATCATGTTACTTTTACCATGGAAAATCCGGTGGTATAGTAGTCTCT 425

RESULT 13
US-10-932-182A-82374
; Sequence 82374, Application US/10932182A
; Publication No. US20060046253A1

GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHIISA
APPLICANT: KODAMA, YUKIO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 82374
LENGTH: 468
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-82374

Query Match 7.5%; Score 53.4; DB 9; Length 468;
Best Local Similarity 51.6%; Pred. No. 2.7e-05;
Matches 148; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 142 CATATCAATATATCTGCGCGATCGCTGTAGCCCTGTACATTAATATGAACGPG 201
DB 139 CATACTAATTTGTTTTCTTAATGCTCCAGAGCTTCATGTGACAGCAAAACGGCGTGCA 198

QY 202 GCTATGCCCTTCATGGTTTGATATTATTG---GGCTTTACACAGATTCACAGGAGGATGAA 258
DB 199 TTGATGCCCTGTGGTTTGACATCTGGAATGGATCCCTAGTTTTCACAAAGTTGACAGT 258

QY 259 TCTGGGATTAACAGCAGCAGCAAGAAATATAAAGCTTTTGATTCATCAAGAGTGGAAGAT 318
DB 259 GACGGTTTTATGAATCTTTTGAATCCATAGAAAGACGGTTAAGCAAGAAATTTGATAAA 318

QY 319 GCATTCCTCTTAACAGAAATTTTGGAGGGTTTCTCAGGAGGAGCTTTATCTTTA 378
DB 319 GGAATTAACCGAGCAGATTTATTCGGAGGTTTCTCAGGAGGCGCCGATTAGCTCTC 378

QY 379 TATATCGCCCTTACCACAGCAGCAAACTGGCAGGTGTCACTGCACT 425
DB 379 GCAACATGATTTACTTTTACATGGAATAATCGGTGGTATAGTAGCTCT 425

RESULT 14
US-10-995-561-255
Sequence 255, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 255
LENGTH: 8098
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-255

Query Match 5.3%; Score 37.6; DB 8; Length 8098;
Best Local Similarity 55.8%; Pred. No. 5.2;
Matches 70; Conservative 1; Mismatches 55; Indels 0; Gaps 0;

QY 569 AAACATTGGTGAATCCAGCAATGTGACCTTTTAAACCTATGAAGGTATGATGCACAGTT 628
DB 1981 AAACCTGGGCACCTAATAGACAGTTACCTCTCCAGCCATTGATCATGAGCAGCTCAGGC 2040

QY 629 CGTGTCAACAGGAAATGATGGATGTCAAGCAATTCATGATAAACTCTACCTCCCAATTG 688

Db 2041 AGCAACAAGAGGAATGAGGCAATTAAGGGAATCTATTGCTGAACACAAACCTCATATTG 2100

QY 689 ATTGAC 694
Db 2101 ACAAAAC 2106

RESULT 15
US-10-995-561-261
Sequence 261, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 261
LENGTH: 10407
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-261

Query Match 5.3%; Score 37.6; DB 8; Length 10407;
Best Local Similarity 55.6%; Pred. No. 5.9;
Matches 70; Conservative 1; Mismatches 55; Indels 0; Gaps 0;

QY 569 AAACATTGGTGAATCCAGCAATGTGACCTTTTAAACCTATGAAGGTATGATGCACAGTT 628
DB 4480 AAACCTGGGCACCTAATAGCAGAGTTACCTCTCCAGCCATTGATCATGAGCAGCTCAGGC 4539

QY 629 CGTGTCAACAGGAAATGATGGATGTCAAGCAATTCATGATAAACTCTACCTCCCAATTG 688
DB 4540 AGCAACAAGAGGAATGAGGCAATTAAGGGAATCTATTGCTGAACACAAACCTCATATTG 4599

QY 689 ATTGAC 694
DB 4600 ACAAAAC 4605

Search completed: April 14, 2006, 13:43:08
Job time : 670 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 21:10:26 ; Search time 193 Seconds
(without alignments)
523.612 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTPLPAIVPARKA.....COQEMMDVKQFDKLLPPTD 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1208	100.0	230	4	AAB2669 Human bra
2	1204	99.7	230	2	Aay09531 Human lys
3	1204	99.7	230	5	Aau85134 Human lys
4	1204	99.7	230	5	Aau85132 Human lys
5	1204	99.7	230	6	Abr54198 Human NOV
6	1204	99.7	230	7	Ades58736 Human Pro
7	1204	99.7	230	7	Add45662 Human Pro
8	1204	99.7	230	8	Abm80990 Tumour-as
9	1204	99.7	263	3	Aab53451 Human col
10	1204	99.7	275	4	Abg07277 Novel hum
11	1153	95.4	230	6	Abr54196 Human NOV
12	1153	95.4	230	7	Ade47694 Human NOV
13	1153	95.4	230	8	Adj78964 Human NOV
14	1130	93.5	230	5	Aau85133 Mouse lys
15	1125	93.1	230	7	Add45660 Rat Prote
16	1125	93.1	230	7	Ades58734 Rat Prote
17	1121	92.8	215	8	Adr66301 Human pro
18	1121	92.8	215	8	Adr66862 Human pro
19	1121	92.8	215	8	Adx97542 Pancreati
20	1109	91.8	230	5	Aau85136 Mouse lys
21	1098	90.9	214	3	Aay69296 A human l
22	1038	85.9	219	4	Aag75019 Human col
23	1015	84.0	207	2	Aay09530 Human lys
24	926	76.7	182	6	Abr54197 Human NOV

ALIGNMENTS

RESULT 1					
AAB82669					
ID	AAB82669 standard; protein; 230 AA.				
XX					
AC	AAB82669;				
XX					
DT	02-OCT-2001 (first entry)				
XX					
DE	Human brain lysophospholipase.				
XX					
KW	Lysophospholipase; human; brain; lysophospholipid; atherosclerosis;				
KW	hyperlipidaemia; dysrhythmia; myocardial ischaemia; demyelination;				
KW	vasotropic; antiatherosclerotic; antilipaeic; neuroprotective; therapy;				
XX	LysoPLA.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	Active-site	119			
FT	Active-site	174			
FT	Active-site	208			
XX					
PN	WO200155166-A1.				
XX					
PD	02-AUG-2001.				
XX					
PF	28-JAN-2000; 2000WO-US002319.				
XX					
PR	28-JAN-2000; 2000US-00493601.				
XX					
PA	(REGC) UNIV CALIFORNIA.				
XX					
PI	Dennis EA, Wang A;				
XX					
DR	WPI; 2001-483215/52.				
DR	N-PSDB; AAH26336.				
XX					
PT	Novel recombinant lysophospholipid-specific human brain lysophospholipase				
PT	enzyme useful for treating disease states having elevated concentrations				
PT	of lysophospholipids, such as atherosclerosis, hyperlipidemia.				
XX					
PS	Claim 4; Fig 1; 38pp; English.				
XX					
CC	The present sequence is that of human brain lysophospholipid-specific				
CC	lysophospholipase (lysoPLA), a novel member of the K/L hydrolase family				
CC	having a catalytic site composed of Ser-119, Asp-174 and His-208.				
CC	LysoPLAs are critical enzymes that act on biological membranes to				

Aab28796	Human hyd
Adb90828	Human hyd
Adh61149	Human hyd
Abm80034	Tumour-as
Abp97164	Human lys
Adx81014	Myelopero
Adx69346	Human lys
Abp97165	Human lys
Adj70254	Human hea
Adj70305	Human hea
Abb67341	Drosophil
Adn22482	Bacterial
Adn20970	Bacterial
Aay48392	Human pro
Abg07276	Novel hum
Adp30086	Human sec
Adn25880	Bacterial
Adx43891	Bacterial
Adn26600	Bacterial
Adx8574	Bacterial
Ads30648	Bacterial

CC regulate the multifunctional lysophospholipids; increased levels of
 CC lysophospholipids are associated with a host of diseases. The enzyme is
 CC widely distributed in almost all tissues, although levels vary. LysoPLA
 CC cDNA (see AAH26336) was obtained by PCR amplification of human brain cDNA
 CC using primers (see AAH26337-38) based on human sequences identified by
 CC database screening using a mouse sequence. The PCR product was expressed
 CC in *Escherichia coli* BL21 (DE3) cells using vector pET28a(a). The
 CC recombinant LysoPLA protein, which included an N-terminal 6His tag and
 CC thrombin cleavage site, was recovered on an Ni-NTA column. Kinetic
 CC analysis showed that human LysoPLA displays apparent co-operativity and
 CC surface dilution kinetics. The recombinant LysoPLA can be used in the
 CC treatment of disease states having elevated concentrations of
 CC lysophospholipids, such as atherosclerosis, hyperlipidaemia, lethal
 CC dysrhythmia in myocardial ischaemia and segmental demyelination of
 CC peripheral nerves. The LysoPLA may be supplied to the enzyme-deficient
 CC patient by infusion or by gene therapy (both claimed). Also claimed is a
 CC method of inhibiting human brain LysoPLA activity using methyl
 CC arachidonyl fluorophosphates

XX Sequence 230 AA;

Query Match 100.0%; Score 1208; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 8.5e-124;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLLNNVAMPWFDDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VTLLNNVAMPWFDDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSLYTALTTOQKLAGVTALSCWLPPLRASLPQGPFGGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSLYTALTTOQKLAGVTALSCWLPPLRASLPQGPFGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTUNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 230
 DB 181 FGSLTVEKLTUNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 230

RESULT 2
 AAY09531
 ID AAY09531 standard; protein; 230 AA.

XX AAY09531;

XX 19-JUL-1999 (first entry)

XX Human lysophospholipase extended NHLP.

XX Human; lysophospholipase; NHLP; cell proliferation; arteriosclerosis;
 KW atherosclerosis; bursitis; cirrhosis; hepatitis; myelofibrosis;
 KW mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;
 KW polycythaemia vera; psoriasis; primary thrombocytopenia; cancer;
 KW inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;
 KW immune response; ankylosing spondylitis; autoimmune haemolytic anaemia.

XX Homo sapiens.

XX WO9849319-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US008782.

XX 29-APR-1997; 97US-00844120.

XX 12-FEB-1998; 98US-00022940.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Shah P, Murry LE;

XX

DR WPI: 1999-326512/27.

DR N-PSDB; AAH56267.

XX New human lysophospholipase (NHLP) polypeptides and polynucleotides which
 PT identify and encode NHLP.

XX Claim 1; Fig 2; 66pp; English.

XX The present sequence is human lysophospholipase (NHLP). The present
 CC invention also describes a method for treating or preventing a disorder
 CC of cell proliferation (e.g. arteriosclerosis, atherosclerosis, bursitis,
 CC cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis,
 CC paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis,
 CC primary thrombocytopenia, and cancers), inflammation (e.g. Addison's
 CC disease, AIDS, allergies, asthma, atherosclerosis, bronchitis) and a
 CC disorder of the immune response (e.g. AIDS, allergies, ankylosing
 CC spondylitis, autoimmune haemolytic anaemia) by administering an
 CC antagonist to NHLP. NHLP proteins, antagonists, antibodies, agonists,
 CC complementary sequences or vectors may be administered in combination
 CC with other therapeutic agents. Antibodies which specifically bind to NHLP
 CC may be used for the diagnosis of disorders characterized by expression of
 CC NHLP or in assays to monitor patients being treated with NHLP or
 CC agonists. The polynucleotides (PNS) encoding NHLP or fragments may be
 CC used therapeutically. In one aspect, the complement of the
 CC polynucleotides may be used where it would be desirable to block the
 CC transcription of the mRNA. Complementary molecules may be used to
 CC modulate NHLP activity or to achieve regulation of gene activity.
 CC Diagnostically, the PNS may be used to detect and quantitate gene
 CC expression in biopsied tissues in which expression of NHLP may be
 CC correlated with disease

XX Sequence 230 AA;

Query Match 99.7%; Score 1204; DB 2; Length 230;

Best Local Similarity 99.6%; Pred. No. 2.3e-123;

Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLLNNVAMPWFDDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

DB 61 VTLLNNVAMPWFDDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSLYTALTTOQKLAGVTALSCWLPPLRASLPQGPFGGANRDISILOCHGDCDPLVPLM 180

DB 121 GGALSLYTALTTOQKLAGVTALSCWLPPLRASLPQGPFGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTUNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 230

DB 181 FGSLTVEKLTUNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 230

RESULT 3

AAU85134

ID AAU85134 standard; protein; 230 AA.

XX AAU85134;

XX 08-MAY-2002 (first entry)

XX Human lysophospholipase I #2.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antilipaeamic; cardiant; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy.

XX Homo sapiens.

XX WO200210185-A1.

```

XX PD 07-FEB-2002.
XX PF 20-JUL-2001; 2001WO-US022975.
XX PR 31-JUL-2000; 2000US-00629645.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Wyatt JR;
XX WPI; 2002-188720/24.
XX DR N-PSDB; ABK37045.
XX PT Novel antisense compound useful for treating inflammation,
XX PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and
XX PT myocardial ischemia, inhibits lysophospholipase I.
XX PS Disclosure; Page 94-95; 131pp; English.
XX CC The invention relates to an antisense compound (I) 8-30 nucleobases in
XX CC length targeted to a nucleic acid molecule encoding lysophospholipase I
XX CC (II), where (I) specifically hybridises with and inhibits the expression
XX CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
XX CC tissues, and for treating a human having a disease or condition
XX CC associated with Lysophospholipase I e.g. inflammation, hyperlipidaemia,
XX CC and cardiovascular disorders such as atherosclerosis and myocardial
XX CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
XX CC useful for distinguishing functions of various members of a biological
XX CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
XX CC represent lysophospholipase I amino acid sequences of the invention
XX CC
XX SQ Sequence 230 AA;
XX
Query Match 99.7%; Score 1204; DB 5; Length 230;
Best Local Similarity 99.6%; Pred. No. 2.3e-123;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPATVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPATVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60

QY 61 VTLMNVAMPSPWFDIIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLMNVAMPSPWFDIIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSlyTALTTOOKLAGVTALSCWLPRLASLPQGPFGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSlyTALTTOOKLAGVTALSCWLPRLASFPQGPFGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTlVNPANVTFTKTEGMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTlVNPANVTFTKTEGMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 4
AAU85132
ID AAU85132 standard; protein; 230 AA.
XX AC AAU85132;
XX DT 08-MAY-2002 (first entry)
XX DE Human lysophospholipase I #1.
XX KW Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
XX KW antilipaeic; cardiant; lysophospholipase I; inflammation; ischaemia;
XX KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
XX KW antisense gene therapy.
XX OS Homo sapiens.
XX PN WO200210185-A1.

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XX PD 07-FEB-2002.
XX PF 20-JUL-2001; 2001WO-US022975.
XX PR 31-JUL-2000; 2000US-00629645.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Wyatt JR;
XX WPI; 2002-188720/24.
XX DR N-PSDB; ABK37030.
XX PT Novel antisense compound useful for treating inflammation,
XX PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and
XX PT myocardial ischemia, inhibits Lysophospholipase I.
XX PS Disclosure; Page 88-89; 131pp; English.
XX CC The invention relates to an antisense compound (I) 8-30 nucleobases in
XX CC length targeted to a nucleic acid molecule encoding lysophospholipase I
XX CC (II), where (I) specifically hybridises with and inhibits the expression
XX CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
XX CC tissues, and for treating a human having a disease or condition
XX CC associated with Lysophospholipase I e.g. inflammation, hyperlipidaemia,
XX CC and cardiovascular disorders such as atherosclerosis and myocardial
XX CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
XX CC useful for distinguishing functions of various members of a biological
XX CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
XX CC represent lysophospholipase I amino acid sequences of the invention
XX CC
XX SQ Sequence 230 AA;
XX
Query Match 99.7%; Score 1204; DB 5; Length 230;
Best Local Similarity 99.6%; Pred. No. 2.3e-123;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPATVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPATVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60

QY 61 VTLMNVAMPSPWFDIIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLMNVAMPSPWFDIIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSlyTALTTOOKLAGVTALSCWLPRLASLPQGPFGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSlyTALTTOOKLAGVTALSCWLPRLASFPQGPFGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTlVNPANVTFTKTEGMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTlVNPANVTFTKTEGMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 5
ABR54198
ID ABR54198 standard; protein; 230 AA.
XX AC ABR54198;
XX DT 23-JUN-2003 (first entry)
XX DE Human NOV7c protein SEQ ID NO:64.
XX KW Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
XX KW anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
XX KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
XX KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaeic;
XX KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
XX KW congenital heart defect; aortic stenosis; valve disease; transplantation;
XX KW tuberosus sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
XX KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;

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XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 230 AA;

Query Match 99.7%; Score 1204; DB 7; Length 230;
Best Local Similarity 99.6%; Pred. No. 2.3e-123;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MCGNNSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLMNVAMPSPFDDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLMNVAMPSPFDDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOOKLAGVTALSCWPLPLRASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTOOKLAGVTALSCWPLPLRASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCQEQEMDMVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCQEQEMDMVKQFIDKLLPPID 230

RESULT 7
ADD45662
ID ADD45662 standard; protein; 230 AA.
XX
AC ADD45662;
XX
XX 29-JAN-2004 (first entry)
XX Human Protein NP_006321, SEQ ID NO 11330.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS
XX WO2003016475-A2.
PN
XX 27-FEB-2003.
PD
XX 14-AUG-2002; 2002WO-US025765.
PF

XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
FI WPI; 2003-268312/26.
DR GENBANK; NP_006321.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 230 AA;

Query Match 99.7%; Score 1204; DB 7; Length 230;
Best Local Similarity 99.6%; Pred. No. 2.3e-123;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNSTPLPAIVPAARKATAAIVFLHGLDGTGHWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLMNVAMPSPFDDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLMNVAMPSPFDDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOOKLAGVTALSCWPLPLRASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTOOKLAGVTALSCWPLPLRASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCQEQEMDMVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCQEQEMDMVKQFIDKLLPPID 230

RESULT 8
ABM80990
ID ABM80990 standard; protein; 230 AA.
XX

AC ABM80990;
XX 18-NOV-2004 (first entry)
XX Tumour-associated antigenic target (TAT) polypeptide PRO59230, SEQ.2551.
DE
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
XX Homo sapiens.
XX WO2004030615-A2.
XX 15-APR-2004.
XX 29-SEP-2003; 2003WO-US028547.
XX 02-OCT-2002; 2002US-0414971P.
XX (GETH) GENENTECH INC.
XX Wu TD, Zhang Z, Zhou Y;
XX WPI; 2004-347921/32.
XX N-PSDB; ACN38804.
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 2551; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 230 AA;
Query Match 99.7%; Score 1204; DB 8; Length 230;
Best Local Similarity 99.6%; Pred. No. 2.3e-123;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLDGTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLDGTGHWAEAFAGIRSHIKYICPHAPVRP 60
QY 61 VTLLNMNVAMSPWDIIIGLSPDSQDESGIKQAENIKALIDQVKNIGIPSNRIILGGFSQ 120
DB 61 VTLLNMNVAMSPWDIIIGLSPDSQDESGIKQAENIKALIDQVKNIGIPSNRIILGGFSQ 120

QY 121 GGALSLYALTQQKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GGALSLYALTQQKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTILNVPANVTFTYEGMHSSCOQENMDVKQFIDKLLPPID 230
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 FGSLTVEKLTILNVPANVTFTYEGMHSSCOQENMDVKQFIDKLLPPID 230
RESULT 9
AAB53451
ID AAB53451 standard; protein; 263 AA.
XX
XX AAB53451;
XX 09-MAR-2001 (first entry)
XX Human colon cancer antigen protein sequence SEQ ID NO:991.
DE
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder.
XX
XX Homo sapiens.
XX WO200055351-A1.
XX 21-SEP-2000.
XX 08-MAR-2000; 2000WO-US005883.
XX 12-MAR-1999; 99US-0124270P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2000-587534/55.
XX N-PSDB; AAC98208.
XX Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.
XX
XX Claim 11; Page 1568-1569; 2104pp; English.
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 263 AA;
Query Match 99.7%; Score 1204; DB 3; Length 263;
Best Local Similarity 99.6%; Pred. No. 2.8e-123;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLDGTGHWAEAFAGIRSHIKYICPHAPVRP 60

Db 34 MCGNNMSTPLPAIIPAARKATAAIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 93
QY 61 VTLLNNVAMPSPWFDIIGLSPDSQDESGIKQAANIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 94 VTLLNNVAMPSPWFDIIGLSPDSQDESGIKQAANIKALIDQEVKNGIPSNRIILGGFSQ 153
QY 121 GGALSILYALTITQOKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 154 GGALSILYALTITQOKLAGVTALSCWLPRLASFPQGPIGGANRDISILOCHGDCDPLVPLM 213
QY 181 FGSLTVEKLTILVNPANVTFTYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
Db 214 FGSLTVEKLTILVNPANVTFTYEGNMHSSCOQEMMDVKQFIDKLLPPID 263

RESULT 10
ABG07277
ID ABG07277 standard; protein; 275 AA.
XX AC ABG07277;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #7268.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US0083631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR N-PSDB; AAS71484.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 37636; 103pp; English.

XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 275 AA;
Query Match 99.7%; Score 1204; DB 4; Length 275;
Best Local Similarity 99.6%; Pred. No. 3e-123; 1; Indels 0; Gaps 0;
Matches 229; Conservative 0; Mismatches 1;
QY 1 MCGNNMSTPLPAIIPAARKATAAIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 46 MCGNNMSTPLPAIIPAARKATAAIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 105
QY 61 VTLLNNVAMPSPWFDIIGLSPDSQDESGIKQAANIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 106 VTLLNNVAMPSPWFDIIGLSPDSQDESGIKQAANIKALIDQEVKNGIPSNRIILGGFSQ 165
QY 121 GGALSILYALTITQOKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 166 GGALSILYALTITQOKLAGVTALSCWLPRLASFPQGPIGGANRDISILOCHGDCDPLVPLM 225
QY 181 FGSLTVEKLTILVNPANVTFTYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
Db 226 FGSLTVEKLTILVNPANVTFTYEGNMHSSCOQEMMDVKQFIDKLLPPID 275

RESULT 11
ABR54196
ID ABR54196 standard; protein; 230 AA.
XX AC ABR54196;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human NOV7a protein SEQ ID NO:60.
XX
KW Human; NOVX; antiatherosclerotic; hypotensive; cardiac; dermatological;
KW anorectic; immunosuppressive; cytostatic; antidiabetic; antiinfertility;
KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipemic;
KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
KW congenital heart defect; aortic stenosis; valve disease; transplantation;
KW tuberosus sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
KW fertility; haemophilia; hypercoagulation; graft versus host disease;
KW idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
KW Crohn's disease; multiple sclerosis; infectious disease; cancer;
KW cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia;
KW metabolic syndrome X.
XX
OS Homo sapiens.
XX
PN WO2003023001-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028538.
XX
XX 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318184P.
PR 10-SEP-2001; 2001US-0318430P.
PR 17-SEP-2001; 2001US-0322636P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 17-SEP-2001; 2001US-0322817P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 14-DEC-2001; 2001US-0341144P.

PR 26-FEB-2002; 2002US-0359599P.
PR 05-MAR-2002; 2002US-0361663P.
PR 03-MAY-2002; 2002US-0377908P.
PR 17-MAY-2002; 2002US-0381483P.
PR 29-MAY-2002; 2002US-0383863P.
PR 02-JUL-2002; 2002US-0393332P.
PR 17-JUL-2002; 2002US-0396412P.
PR 13-AUG-2002; 2002US-0403517P.
PR 06-SEP-2002; 2002US-00236417.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
PI Crabtree J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K;
PI Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
PI Kekuda R, Khrantsov NV, Leach MD, Lepley DM, Li L, Liu X;
PI Malvanekar UM, Miller CE, Ooi T, Padigar M, Patturajan M;
PI Pena CE, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA;
PI Spaderna SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ;
PI Zerhusen BD, Zhong M;
XX
XX WPI; 2003-313241/30.
DR N-PSDB; ACC62265.
XX
XX Novel human proteins and nucleic acid encoding the proteins, useful for
PT diagnosis, treatment and prevention of disorders involving the human
PT protein or nucleic acid e.g. cardiac and neurological disorders.
XX
XX Claim 1; Page 129; 460pp; English.
XX
CC The present invention describes isolated human NOVX proteins, where X is
CC 1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
CC ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiac,
CC hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
CC antidiabetic, antifertility, haemostatic, antiinflammatory, cytostatic,
CC antiasthmatic, metabolic, immunomodulator, neuroprotective, nontropic,
CC antiparkinsonian and antilipaeamic activities, and can be used in gene
CC therapy. NOVX proteins are useful for treating or preventing a pathology
CC associated with a NOVX protein in humans and for treating a syndrome
CC associated with the human disease. NOVX nucleic acids, proteins and
CC antibodies can be used in the treatment and diagnosis of cardiomyopathy,
CC atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
CC valve disease, tuberosclerosis, scleroderma, obesity, transplantation,
CC congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
CC disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
CC disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, dyslipidaemias, and metabolic syndrome X.
CC ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
CC sequences, which are used in examples from the present invention.
CC ABR54277 represents a human trypsinogen protein given in comparison with
CC the human NOV35b protein in the exemplification of the present invention
XX
XX Sequence 230 AA;
XX

Query Match 95.4%; Score 1153; DB 6; Length 230;
Best Local Similarity 94.8%; Pred. No. 9.4e-118;
Matches 218; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 MCGNNMSTLPAIVPAARAKATAAIVLHGLDGTGHCWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSTLPTTIVPAARAKATTEVIFLHGLDGTGHCWAEAFAGITSSHIKYICPHAPVRP 60
QY 61 VTLLNNMAMPSWFDIIGLPSDSESGIKQAENIKALIDQVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNNMAMPSWFDIIGLPSDSESGIKQAENIKALIDQVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYLTATTOQKLAGVTALNSCWLPRLRASLPQGPFGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSLYLTATTHOKLAGVTALNSCWLPRLWASFPQGPFGANRDISILQCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTILNPNANVTFTKTEGMHSSCOQEMDMVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTILNPNANVTFTKTEGMHSSCOQEMDMVKQFIDKLLPPID 230
RESULT 12
ADE47694
ID ADE47694 standard; protein; 230 AA.
XX
XX ADE47694;
XX
XX 29-JAN-2004 (first entry)
XX Human NOV18a protein SEQ ID NO:56.
XX human; cardiac; antiarteriosclerotic; hypotensive; immunosuppressive;
KW dermatological; anorectic; cytostatic; antidiabetic; haemostatic;
KW anti-HIV; antiasthmatic; antibacterial; virucide; neuroprotective;
KW nontropic; antiparkinsonian; antilipaeamic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO2003076642-A2.
XX
XX 18-SEP-2003.
XX
XX 02-AUG-2002; 2002WO-US024459.
XX
XX 02-AUG-2001; 2001US-030501P.
XX 03-AUG-2001; 2001US-0310291P.
XX 08-AUG-2001; 2001US-0310951P.
XX 09-AUG-2001; 2001US-0311292P.
XX 13-AUG-2001; 2001US-0311979P.
XX 14-AUG-2001; 2001US-0312203P.
XX 17-AUG-2001; 2001US-0313156P.
XX 17-AUG-2001; 2001US-0313201P.
XX 20-AUG-2001; 2001US-0313702P.
XX 21-AUG-2001; 2001US-0314031P.
XX 23-AUG-2001; 2001US-0314466P.
XX 28-AUG-2001; 2001US-0315403P.
XX 29-AUG-2001; 2001US-0315853P.
XX 31-AUG-2001; 2001US-0316508P.
XX 31-SEP-2001; 2001US-0323936P.
XX 03-DEC-2001; 2001US-0338078P.
XX 05-FEB-2002; 2002US-0354655P.
XX 05-MAR-2002; 2002US-0361764P.
XX 19-APR-2002; 2002US-0373825P.
XX 15-MAY-2002; 2002US-0380971P.
XX 16-MAY-2002; 2002US-0380980P.
XX 28-MAY-2002; 2002US-0381039P.
XX 29-MAY-2002; 2002US-0383761P.
XX 01-AUG-2002; 2002US-0383887P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Zerhusen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;
PI Pena CE, Shimkets RA, Li L, Berghs C, Zhong M, Casman SJ, Voss EZ;
PI Boldog FL, Padigar M, Smithson G, Shenoy SG, Ji W, Gorman L;
PI Vernet CAM, Leite MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;
PI Burgess CE, Khrantsov NV, Ort T, Ellerman K, Rastelli L, Agee ML;
PI Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eisen A, Gangolli EA;
PI Giot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalte T, Liu X;
PI Taupier RJ, Catterton E;
XX
XX WPI; 2003-779062/73.
DR N-PSDB; ADE47693.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, tissue typing
PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
PT or pharmacogenomics.

XX Claim 1; SEQ ID NO 56; 562bp; English.

XX The invention relates to a novel (NOVX) human polypeptide. A polypeptide

XX of the invention has cardiac, antiarteriosclerotic, hypotensive,

XX immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,

XX haemostatic, anti-HIV, antisthmatic, antibacterial, virucide,

XX neuroprotective, neurotropic, antiparkinsonian, and antilipase activity.

XX A polynucleotide encoding a polypeptide of the invention may have a use

XX in gene therapy, and as a vaccine. A polypeptide of the invention is

XX useful in the manufacture of a medicament for treating a syndrome

XX associated with a human disease, the disease selected from a pathology

XX associated with the polypeptide. These may also be used in diagnosing,

XX treating or preventing NOVX-associated disorders such as cardiomyopathy,

XX atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,

XX haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,

XX multiple sclerosis, infections, anorexia, cancer-associated cachexia,

XX neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's

XX disease), haematopoietic disorders, dyslipidaemias and other wasting

XX disorders associated with chronic diseases. The nucleic acids are also

XX used as hybridisation probes, in chromosome mapping, tissue typing,

XX preventive medicine, and pharmacogenomics. The polypeptides are also

XX useful as vaccines. The present sequence represents a NOVX polypeptide of

XX the invention.

SQ Sequence 230 AA;

Query Match 95.4%; Score 1153; DB 7; Length 230;

Best Local Similarity 94.8%; Pred. No. 9.4e-118;

Matches 218; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLIGDTGHCWAFAFAGIRSHIKYICPHAPVRP 60

DB 1 MCGNNMSTPLPAIVPAARKATTEVFLHGLIGDTGHCWAFAFAGIRSHIKYICPHAPVRP 60

QY 61 VTLLNNVAMPSPFDITGLSPDSDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

DB 61 VTLLNNIAMPSPFDITGLSPDSDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSILYALTTHOKLAGVTALNCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180

DB 121 GGALSILYALTTHOKLAGVTALNCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTLLNPNANVTFTYEGNMHSSCQEMMDVKQFIDKLLPPID 230

DB 181 FGSLTVEKLTLLNPNANVTFTYEGNMHSSCQEMMDVKQFIDKLLPPID 230

RESULT 13

ADJ78964

ID ADJ78964 standard; protein; 230 AA.

XX ADJ78964;

XX ADJ78964;

XX 06-MAY-2004 (first entry)

XX Human NOVX protein Nov18A amino acid sequence.

XX NOVX; cytostatic; antidiabetic; anorectic; cerebroprotective;

XX neuroprotective; antiinflammatory; thyromimetic; cardiac; gene-therapy;

XX antitense-therapy; cancer; diabetes; obesity; endocrine disorder;

XX CNS disorder; cardiovascular disorder; inflammatory disorder;

XX detection assay; screening assay; chromosome mapping; tissue typing;

XX predictive medicine; human; Nov18A.

XX Homo sapiens.

XX US2004014053-A1.

XX 22-JAN-2004.

XX 01-AUG-2002; 2002US-00210130.

XX

PR 02-AUG-2001; 2001US-0309501P.

PR 03-AUG-2001; 2001US-0310291P.

PR 08-AUG-2001; 2001US-0310951P.

PR 09-AUG-2001; 2001US-0311292P.

PR 13-AUG-2001; 2001US-0311979P.

PR 14-AUG-2001; 2001US-0312203P.

PR 17-AUG-2001; 2001US-0313156P.

PR 17-AUG-2001; 2001US-0313201P.

PR 20-AUG-2001; 2001US-0313643P.

PR 20-AUG-2001; 2001US-0313702P.

PR 21-AUG-2001; 2001US-0314031P.

PR 23-AUG-2001; 2001US-0314466P.

PR 28-AUG-2001; 2001US-0315403P.

PR 29-AUG-2001; 2001US-0315853P.

PR 31-AUG-2001; 2001US-0316508P.

PR 17-SEP-2001; 2001US-0322716P.

PR 21-SEP-2001; 2001US-0323936P.

PR 03-DEC-2001; 2001US-0338078P.

PR 05-FEB-2002; 2002US-0354655P.

PR 05-MAR-2002; 2002US-0361764P.

PR 19-APR-2002; 2002US-0373825P.

PR 15-MAY-2002; 2002US-0380971P.

PR 16-MAY-2002; 2002US-0380980P.

PR 28-MAY-2002; 2002US-0381039P.

PR 29-MAY-2002; 2002US-0383761P.

PR 29-MAY-2002; 2002US-0383887P.

XX

PA (ZERH/) ZERHUSEN B D.

PA (PATT/) PATTURAJAN M.

PA (KEKU/) KEKUDA R.

PA (MILL/) MILLER C E.

PA (RIEG/) RIEGER D K.

PA (PENA/) PENNA C E A.

PA (SHIM/) SHIMKETS R A.

PA (LILL/) LI L.

PA (BERG/) BERGHS C.

PA (ZHON/) ZHONG M.

PA (CASN/) CASMAN S J.

PA (VOSS/) VOSS E Z.

PA (BOLD/) BOLDOG F L.

PA (PADI/) PADIGARU M.

PA (SMIT/) SMITHSON G.

PA (JIMW/) JI W.

PA (GORM/) GORMAN L.

PA (VERN/) VERNET C A M.

PA (LEIT/) LEITE M W.

PA (GUOX/) GUO X S.

PA (ANDE/) ANDERSON D W.

PA (SPYT/) SPYTEK K A.

PA (GERL/) GERLACH V.

PA (BURG/) BURGESS C E.

PA (KHRA/) KHRAMTSOV N V.

PA (ORTT/) ORT T.

PA (ELLE/) ELLERMAN K.

PA (RAST/) RASTELLI L.

PA (AGEE/) AGE E M L.

PA (CHAU/) CHAUDHURI A.

PA (CHAN/) CHANT J S.

PA (DIPI/) DIPPO V A.

PA (EDIN/) EDINGER S R.

PA (EISE/) EISEN A J.

PA (GANG/) GANGOLLI E A.

PA (GIOT/) GIOT L.

PA (OOIC/) OOI C E.

PA (ROTH/) ROTHENBERG M E.

PA (SPAD/) SPADERNA S K.

PA (HJAL/) HJALT T.

PA (LIUX/) LIU X.

PA (TAUP/) TAUPIER R J.

PA (CATT/) CATTERTON E.

PA (SHEN/) SHENOY S G.

XX

Zerhusen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;

PI Pena CEA, Shimkets RA, Li L, Berghs C, Zhong M, Casman SJ, Voss EZ;
PI Boldog FL, Padigaru M, Smithson G, Ji W, Gorman L, Vernet CAM;
PI Leite MW, Guo XS, Anderson DW, Spytek KA, Gerlach V, Burgess CE;
PI Khrantsov NV, Ort T, Ellerman K, Rastelli L, Agee ML, Chaudhuri A;
PI Chant JS, Dipippo VA, Edinger SR, Eisen AJ, Gangolli EA, Giot L;
PI Ooi CE, Rothenberg ME, Spaderna SK, Hjalt T, Liu X, Taupier RJ;
PI Catterton E, Shenoy SG;
XX WPI; 2004-108206/11.
DR N-PSDB; ADJ78963.
XX

XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.

XX Claim 1; SEQ ID NO 56; 250bp; English.

XX This invention relates to a novel isolated NOVX polypeptide comprising a
CC fully defined sequence of, a mature form, one or more conservative
CC substitutions or at least 95% identity to 247 amino acids as given in the
CC specification. The invention may be useful for the development of
CC compounds with a cytostatic, antidiabetic, anorectic, cerebroprotective,
CC neuroprotective, antiinflammatory, thyromimetic or cardiact activity. In
CC addition, the disclosed sequences may prove useful for gene-therapy or
CC antisense-therapy. The invention may be useful for the diagnosis and
CC treatment of disorders associated with aberrant expression or activity of
CC the NOVX polypeptide, such as cancer, diabetes, obesity, and endocrine,
CC CNS, cardiovascular and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. The present sequence is that of a human NOVX
CC protein of the invention.

XX SQ Sequence 230 AA;

Query Match 95.4%; Score 1153; DB 8; Length 230;
Best Local Similarity 94.8%; Pred. No. 9.4e-118;
Matches 218; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSTPLTIVPAARKATTEVIFLHGLGDTGHWAEAFAGIITSSHIKYICPHAPVRP 60
QY 61 VTILNMVAMPWFDDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTILNMVAMPWFDDIIGLSPDSQDESGIKQAAQNTKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSITYALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSITYALTTHQKLAGVTALNCWLPRLWASFPQGPPIGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKTYEGNMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLKTLVNPANVTFTKTYEGNMHSSCCQEMMNKQFIDKLLPPID 230

RESULT 14
AAU85133
ID AAU85133 standard; protein; 230 AA.

XX AAU85133;

XX 08-MAY-2002 (first entry)

XX Mouse lysophospholipase I #1.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
KW antilipemic; cardiact; lysophospholipase I; inflammation; ischaemia;
KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
KW antisense gene therapy.
XX Mus musculus.

PN WO200210185-A1.
XX 07-FEB-2002.
PD 20-JUL-2001; 2001WO-US022975.
XX 31-JUL-2000; 2000US-00629645.
XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

XX WPI; 2002-188720/24.

XX N-PSDB; ABK37037.

XX Novel antisense compound useful for treating inflammation,
PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and
PT myocardial ischemia, inhibits lysophospholipase I.

XX Disclosure; Page 92-93; 131pp; English.

XX The invention relates to an antisense compound (I) 8-30 nucleobases in
CC length targeted to a nucleic acid molecule encoding lysophospholipase I
CC (II), where (I) specifically hybridises with and inhibits the expression
CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
CC tissues, and for treating a human having a disease or condition
CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
CC and cardiovascular disorders such as atherosclerosis and myocardial
CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
CC useful for distinguishing functions of various members of a biological
CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
CC represent lysophospholipase I amino acid sequences of the invention

XX SQ Sequence 230 AA;

Query Match 93.5%; Score 1130; DB 5; Length 230;
Best Local Similarity 91.3%; Pred. No. 3.2e-115;
Matches 210; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIKSPHIKYICPHAPVRP 60
QY 61 VTILNMVAMPWFDDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTILNMVAMPWFDDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSITYALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSITYALTTOOKLAGVTALSCWLPRLASFSQGPINSANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKTYEGNMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVERLKALINPANVTFTKTYEGNMHSSCCQEMMDVKRHFIDKLLPPID 230

RESULT 15
ADD45660
ID ADD45660 standard; protein; 230 AA.

XX ADD45660;

XX 29-JAN-2004 (first entry)

XX Rat Protein NP_037138, SEQ ID NO 11328.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CGI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 21:14:16 ; Search time 40 Seconds
(without alignments)
553.246 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTLPAIPAARXA.....CQEMMDVKQFDKLLPPID 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510.5	42.3	333	2 T23324	hypothetical prote
2	471	39.0	247	2 T52511	related to lysopho
3	371.5	30.8	224	2 T39158	lysophospholipase
4	356	29.5	227	2 S64955	probable membrane
5	326.5	27.0	224	2 H82658	carboxylesterase x
6	279	23.1	218	2 JU0277	carboxylesterase (
7	274	22.7	215	2 A83163	probable carboxyle
8	272	22.5	218	2 JQ0885	esterase A (EC 3.1
9	271.5	22.5	471	2 T04911	hypothetical prote
10	183	15.1	161	2 C96568	hypothetical prote
11	167.5	13.9	126	2 D96518	protein T256.14 [i
12	164.5	13.6	204	2 S75304	serine esterase -
13	153	12.7	200	2 G96550	hypothetical prote
14	152.5	12.6	207	2 S43880	esterase - Spiruli
15	151	12.5	214	2 AB2195	serine esterase [i
16	149	12.3	197	2 A96568	hypothetical prote
17	147	12.2	197	2 B96568	hypothetical prote
18	147	12.2	241	2 T39231	probable lysophosp
19	124.5	10.3	243	2 G86524	lysophospholipase
20	124.5	10.3	243	2 D72098	serine esterase, p
21	123.5	10.2	305	2 T20470	hypothetical prote
22	120	9.9	304	2 D86998	probable secreted
23	117	9.7	304	2 C70982	probable lpqC prot
24	111	9.2	239	2 F81704	serine esterase, p
25	110.5	9.1	204	2 F83921	hypothetical prote
26	107.5	8.9	395	2 F72424	hypothetical prote
27	103	8.5	319	2 AB1334	hypothetical prote
28	102.5	8.5	215	2 D71634	hypothetical prote
29	101.5	8.4	219	2 A70734	probable cutinase

30	101.5	8.4	243	2 C95908	hypothetical prote
31	101	8.4	378	2 T41456	probable phosphol
32	100.5	8.3	216	2 C97843	serine esterase ho
33	98.5	8.2	240	2 G91045	hypothetical prote
34	98.5	8.2	240	2 C85890	hypothetical prote
35	98	8.1	335	2 T20465	hypothetical prote
36	97.5	8.1	284	2 S17820	protoporphyrin IX
37	97	8.0	433	2 A39556	triacylglycerol li
38	95	7.9	416	2 D70347	cell division prot
39	95	7.9	655	2 T34219	hypothetical prote
40	94	7.8	414	2 S39530	poly(3-hydroxybuty
41	93.5	7.7	240	2 H65022	hypothetical prote
42	92.5	7.7	239	2 A71552	probable lysophosp
43	92	7.6	276	2 A55211	chloride peroxidase
44	92	7.6	656	2 E96713	hypothetical prote
45	91	7.5	250	2 AF1357	hypothetical prote

ALIGNMENTS

RESULT 1

T23324

hypothetical protein K04G2.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T23324

R;Gardner, A.

submitted to the EMBL Data Library, July 1996

A;Reference number: Z19727

A;Accession: T23324

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-333 <WIL>

A;Cross-references: UNIPROT:Q21224; UNIPARC:UPI000017BA8D; EMBL:Z75712; PIDN:CAB00042.1

A;Experimental source: Clone K04G2

C;Genetics:

A;Gene: CESP:K04G2.5

A;Map position: 1

A;Introns: 8/1; 54/1; 87/1; 165/2; 263/3; 318/3

Query Match 42.3%; Score 510.5; DB 2; Length 333;
Best Local Similarity 49.3%; Pred. No. 7e-40;
Matches 106; Conservative 29; Mismatches 71; Indels 9; Gaps 5;

QY	11	PAIVPAARKATAAAVIFLHGLGDTGHGWAAP-AGIRSSHIKICPHAPVRPVTINMNVAM	69
DB	119	PSIVSPRGHKGTILFLHGLDQGHGWAFAFKTEAKHDNIKFCPHSSRPVTINMGMRM	178
QY	70	PSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTA	129
DB	179	PAWFDLFLGLDPAQDEQGINRATQYVHQLIDAEVAAGIPASRIAVGFGSMGALAIYAG	238
QY	130	LTQQKLAGVTALSCLWPLRASLPQGPIGG--ANRDISILOCHDCDPLVPLMFGSLTVE	187
DB	239	LTYPQKLGIVGLSFFLQTKTFP-----GSFTANNATPIFLGHGTDPLFLPFGQMSQ	294
QY	188	KLKTLVNPANVTFTYEGHMHSSCQCEEMMDVKQFI	222
DB	295	YIKKF-NP-KVELHTYRGHQHSSCGEEMDRDVKTF	327

RESULT 2

T52511

related to lysophospholipase [imported] - Neurospora crassa

N;Alternate names: protein B2523.70

C;Species: Neurospora crassa

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C;Accession: T52511

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura

submitted to the Protein Sequence Database, September 2000

A;Reference number: Z26053

A;Accession: T52511

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <SCH>
A;Cross-references: UNIPROT:Q9HFJ5; UNIPARC:UPT000001796CD; EMBL:AL442164; GSPDB:GN000116;
A;Experimental source: BAC clone B2J23; strain OR74A
C;Genetics:
A;Gene: NCSP:B2J23.70
A;Map position: 6
A;Introns: 85/2; 212/2

Query Match	39.0%;	Score 471;	DB 2;	Length 247;
Best Local Similarity	42.4%;	Fred. No. 2.3e-36;		
Matches	98;	Conservative 40;	Mismatches 79;	Indels 14; Gaps 4

Qy	11	PAIVPAARKATAAATVIFLHGLGDTGHGWAEAFAGIRS----	SHIKVICHPAPVRPVTLLNNN	66
Db	9	PLLVPAVARHTATVIFLHGLGDTGHGWASAVEQWERRQRLDEVKFLPHAPSIPITANWG		68
Qy	67	VAMPSWFIIIGLSPDS-----	QDESGIQKAENIKALIDQEVKNGIPSNRIILGGFS	119
Db	69	MKMPGWYDIVSLPTYSAEALRRNDEAGIILTSQAYFHDLLQKEIDSGIPADRIVIGFS		128
Qy	120	OGGALSALTALTTOOKLAGVTALSCWLPURASLPQ-GPIGGANRDISILQCHGDCDPLVP		178
Db	129	OGGANGLPSGLTAKCKLAGIILTSYLLLSLKFAELVPKPEFKETPIFMAHGDDAPVN		188
Qy	179	LMGSLTVEKLKTLVNPANVTFTKTYEGVMHSSCQOEMMDVVKQFIDKLPLPI		229
Db	189	YKLGTMTRDLLEKEM--GYNVKFTPTYPGMHGSAELDAIEDFLTERLPKV		237

RESULT 3
T39158
lysophospholipase - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39158
R:McLean, J.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z18131
A:Accession: T39158
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-224 <MCL>
A:Cross-references: UNIPROT:O42881; UNIPARC:UPI000006AD33; EMBL:AL021817; PIDN:CAAL17025
A:Experimental source: strain 972h; cosmid c8E11
C:Genetics:
A:Gene: SPDB:SPAC8E11.04c
A:Map position: 1
A:Introns: 25/1; 53/2; 69/2; 118/1

Query Match	30.8%;	Score 371.5;	DB 2;	Length 224;
Best Local Similarity	39.9%;	Pred. No. 4e-27;		
Matches	85;	Conservative 41;	Mismatches 72;	Indels 15; Gaps 6
Qy	21	TAAVFLHGLGDTGHW---	AEAPAGIRSSHIKICYPAPVPVTLNNVMWPSWFDIIG	77
Db	17	TATVIFLHGLGDSGGGSMFMTWSNFK--	HKWIFPNAPSIPVTVNNGKMPAMVDIYS	74
Qy	78	LSPSQBEDSGIKAAENIKALIDOEKNGIPSNRIILGGFSGGALSILYALTITQOOLA	137	
Db	75	FADMKREDENGILRSAGQLHELIDAEALGIPSDRILGGFSGGCMVSLYAGLTYPKRLA	134	
Qy	138	GVTALSCWLPKRASLPQGPICGANDRISITLOCHGDCDPLVPLMFGLSTVEKRLTLVNNPAN	197	
Db	135	GIMHSGGFELPASKFPSA--LSRVAKEIPILLITYMTEDPIVPSVLSSASA--	KYLIN--N 188	
Qy	198	VTFK-----TYEGMHSSCQEQEMVVKQFIDKLL	226	
Db	189	LOLKCLDRPFEGDAHLSSESFMAMVKFTQTVI	221	

RESULT 4

S64955
probable membrane protein YJR118c - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein L2955
C;Species: *Saccharomyces cerevisiae*
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: S64955; S69406
R;Verhaesselt, P.; Voet, M.; Voickaert, G.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64943
A;Accession: S64955
A;Molecule type: DNA
A;Residues: 1-227 <VER>
A;Cross-references: UNIPROT:Q12354; UNIPARC:UPI000006C16B; EMBL:Z73290; NID:g1
R;Verhaesselt, P.; Voickaert, G.
submitted to the EMBL Data Library, September 1995
A;Reference number: S69393
A;Accession: S69406
A;Molecule type: DNA
A;Residues: 1-227 <VSW>
A;Cross-references: UNIPARC:UPI000006C16B; EMBL:X89514; NID:g1297019; PID:e198
C;Genetics:
A;Cross-references: SGD:S0004108
A;Map position: 12R
C;Keywords: transmembrane protein
C;136-152/Domain: transmembrane #status predicted <TWM>

Query Match	29.5%	Score 356;	DB 2;	Length 227;
Best Local Similarity	37.4%;	Pred. No. 1.2e-25;		
Matches	82;	Conservative	29;	Mismatches 90; Indels 18; Gaps 4
Qy	20	ATAAVIFLHGLGDTGHGWA-----BAFAGIRSHIKYICPHAFVPRVVTILMNVA	68	
Db	13	ARQTIIIFLHGLGDTSGWGFLAQYLQORDPAF-----QHTNFVFPNAPELHVTGTANGGAL	67	
Qy	69	MPSWFDIIGLSPD--SQEDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGNLSLY	127	
Db	68	MPAWFDILEWDPSPFSKVDSDGFMSNLSIEKTVKQEIIDKGIKPEQIIIGGFSQGGNLSLY	127	
Qy	128	TALTTQOKLAGVTALSCWLPURASLPQGPFGAGNRDISILOCHGBCDPLVPLMFGSLTVE	187	
Db	128	TSVTLPLPWKIGIVALSFGFCSIPGLIKQHK-NGINVKPTIFHCHGDMDPVVPGLGLIKAKQ	186	
Qy	188	KLKTLVNPANVFTKTYEGMMHSSCQEQEMMDVKQFIDKLL	226	
Db	187	FYQDSCEITONYEFKVKYKGMASHSTVPDELEDLASFIKKSL	225	

RESULT 5
H82658
carboxylesterase XF1624 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82658
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleot
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82658
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <SIM>
A:Cross-references: UNIPROT:Q9PCV0; UNIPARC:UPI00000C27A6; GB:AE003989; GB:AE0
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvare
Briões, M.R.S.; Bueno, C.M.R.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.;
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.;
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miy
submitted to GenBank, June 2000

probable carboxylesterase PA3959 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: A83163
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brodey, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; L
y, Lory, S.; Olson, M.V.
NA:Date: 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Residues: 1-215 <ST0>

8709

Best Local Similarity 35.6%; Pred. No. 4.9e-18;

[illegible]

63 I.NMNVAMPWFEDIIGLSPDSEDESGIKOAAENIKALIDQEVKNIGIPSNRIILGGFSOGG 122

181

DB J/4 GRAAHDAU--AQGVGVGWHUIP-NGHEVSVLEEIHDIIGAWJKNKE ZTJ

700885

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

SUBMITTED TO OFFICE, DATE: 2002
 REFERENCE NUMBER: 700885

A;Residues: 1-218 <YUF>

1. General: 001

Query Match 22.5%; Score 272; DB 2; Length 218;

11 D A T I O M A B K A T A A Y I E I H C I G D T C H C W A F A F A G T P S S H T - - K V T C P H A P V R P V T L N M N V A 68

06 64 MFSWIDTANMZFANKSTDBBEEETUHMVTDZTEVQXKTCOTDZSUKLZSUCN

124 AFKKWEGPLGGVIALSTYAPTFDNDLQ--LSASQQRIP^TCLHGGYDEVVQNAMGRSAYE 181

A;Cross-references: UNIPROT:P73192; UNIPARC:UPI00000D338C; EMBL:D90904; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 13.6%; Score 164.5; DB 2; Length 204;
Best Local Similarity 28.7%; Pred. No. 7.7e-08;
Matches 62; Conservative 41; Mismatches 88; Indels 25; Gaps 10;

QY 9 PLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRPVTLMNVVA 68
DB 11 PDPAVTPT--DSSYLLVMLHGWGADARDLSLAPMLDLPNYQWRVFNAPFTHPQIPOGRA 68

QY 69 MFSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSIIY 127
DB 69 ---WYDL-----ESQNF-GLAQARQGLRAYLLGLAEETGIPLARTILGGFSQGGAMALD 119

QY 128 TALTTOQKLAGVTALSCWPLR-ASLPOGPPIGGANRDISILOCHGDCDPLVPLMFGSLTV 186
DB 120 VGLTL--PLAKFSLSGYLHFQESQPA-----IAPILLIHGTEDPVPLRMAQQA 170

QY 187 EKLKTLVNPANVTFTYEGMHSSCOQEMMDVKQFI 222

DB 171 AELESI--GASVEYQEP-MGHAIPPMALARKSFL 203

RESULT 13

G96550
hypothetical protein Film15.15 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: G96550

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

aneen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Liu, Y.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G96550

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-200 <STO>

A;Cross-references: UNIPROT:Q9SYD1; UNIPARC:UPI00000A181C; GB:AE005173; NID:g4836939; P

C;Genetics:

A;Gene: Film15.15

A;Map position: 1

Query Match 12.7%; Score 153; DB 2; Length 200;
Best Local Similarity 28.7%; Pred. No. 8.9e-07;
Matches 43; Conservative 30; Mismatches 53; Indels 24; Gaps 7;

QY 13 IVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRPVTLMNVAM--- 69
DB 30 VTPARH-QATIVLWLDHNSGYDSSELYKVSFLYVNVKICPSSP-----LISNVGFGGA 83

QY 70 --PSWFDIIGLS---PDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGAL 124
DB 84 PARAWFKVNEFSSRPDPYEME-GLKNSAAHVAGLLKNPENVMKG-----VAGYGIGGAL 138

QY 125 SLYTAL-----TTQOKLAGVTALSCWPLR 149

DB 139 ALHIATCYALGSPFIQIRAVGVINCWLPNR 168

RESULT 14

S43880

esterase - Spirulina platensis

C;Species: Spirulina platensis

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S43880

R;Salvi, S.; Trinei, M.; Lanfaloni, L.; Pon, C.L.

Mol. Gen. Genet. 243, 124-126, 1994

A;Title: Cloning and characterization of the gene encoding an esterase from Spirulina p

A;Reference number: S43880; MUID:94247351; PMID:8190066

A;Accession: S43880

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-207 <SAL>

A;Cross-references: UNIPROT:Q53415; UNIPARC:UPI00000B29D2; GB:S70419; NID:g546788; PIDN

Query Match 12.6%; Score 152.5; DB 2; Length 207;

Best Local Similarity 29.4%; Pred. No. 1e-06;

Matches 62; Conservative 28; Mismatches 88; Indels 33; Gaps 10;

QY 24 VIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRPVTLMNVAMP---SWFDIIGLSP 80

DB 20 IIFLHGWGANCBDLTFAPMLRLPNYWFEPPEAPF-----PHPOVPGGRAWYAL----- 68

QY 81 DSOEDSGIKQAENIKALIDQ-----EVKNGIPSNRIILGGFSQGGALSlyTALTTOQKL 136

DB 69 ETQEYE-GIBESREK---LIDMLNIAQTGTTPORTILGGFSQGGAMTFDVGR--MGF 122

QY 137 AGVTALSCWPLRASILPOGPPIGGANRDISILOCHGDCDPLVPLMFGSLTVKLTALVNP 196

DB 123 AGLIVLGVLFHKPEFPQQTPLP-----PILWAHGKQDMVVLGAHAHQARDSFQKL--GA 174

QY 197 NVTFKTYEGMHSSCOQEMMDVKQFIDKLLP 227

DB 175 TVEYHEY-NMGHEICPDILGLIQSFVKTLP 204

RESULT 15

AB2195
serine esterase [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AB2195

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata,

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AB2195

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-214 <KUR>

A;Cross-references: UNIPROT:Q8YSH2; UNIPARC:UPI00000CE692; GB:BA000019; PIDN:BA074812.1

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all3113

Query Match 12.5%; Score 151; DB 2; Length 214;

Best Local Similarity 28.4%; Pred. No. 1.5e-06;

Matches 65; Conservative 33; Mismatches 93; Indels 38; Gaps 12;

QY 7 STPLP---AIVPAARKATAA--VIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHA---P 57

DB 6 SXPLSIQFTTVTPAKSQTPAGLVVTLHGWANAEDVASLLPYENLPDYQVFVFNAPVPY 65

QY 58 VRPVTLMNVAMPSPFDIIGLSPDSQED--ESGIKQAENIK-ALIDQEVKNGIPSNRIIL 115

DB 66 YAPLG-----RSWYDL-----ROENNYEGLAESRELLKDFVLSLESSTGVPLSRITL 112

QY 116 GGFSGGALSlyTALTTOQKLAGVTALSCWPLRASILPOGPPIGGANRDI--SIQCHGDCD 174

DB 113 SGFSQGGAMTF--DVGSKLPVLGVVNSGVYLHPEALSPD-----NTNPTTILILGTRD 164

QY 175 PLVPLMFGSLTVKLTALVNPANVTFTYEGMHSSCOQEMMDV-KQFI 222

DB 165 EVVPLQ---AAVKARTTVESLGVVPVQYQEFEGAGHEINLEMLNVARNFI 209

Search completed: April 13, 2006, 21:18:40
Job time : 43 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 21:10:56 ; Search time 231 Seconds
(without alignments)
702.474 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTPLPAIVPAARKA.....CQEMWVQKFDKLLPPID 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1204	99.7	230	1 LYPAL HUMAN	O61q08 homo sapien
2	1204	99.7	230	2 O61A01 HUMAN	O61a01 homo sapien
3	1201	99.4	230	2 O5RBR7 PONGY	O5rb07 pongo pygma
4	1130	93.5	230	1 LYPAL MOUSE	P97823 mus muscula
5	1130	93.5	230	1 LYPAL RABIT	O77821 oryctolagus
6	1126	93.2	230	2 O4FK51 MOUSE	O4fk51 mus musculus
7	1125	93.1	230	1 LYPAL RAT	P70470 rattus norv
8	1105	91.5	219	2 O77820 RABIT	O77820 oryctolagus
9	1030	85.3	230	2 O6DJB2 XENTR	O6djb2 xenopus tro
10	1025	84.9	230	2 O6GR07 XENLA	O6gr07 xenopus lae
11	950	78.6	229	2 O4RNO9 TETNG	O4rn09 tetraodon n
12	866.5	71.7	232	2 O6BWM8 BRARE	O6bw08 brachydanio
13	851	70.4	231	1 LYPAL RAT	O9qy18 rattus norv
14	845	70.0	231	1 LYPAL2 MOUSE	O9wt17 mus musculus
15	841	69.6	231	1 LYPAL2 HUMAN	O95372 homo sapien
16	833	69.0	231	2 O6P346 XENTR	O6p346 xenopus tro
17	824	68.2	231	2 O7ZXQ6 XENLA	O7zxq6 xenopus lae
18	819.5	67.8	196	2 O568J5 BRARE	O568j5 brachydanio
19	787	65.1	231	2 O9UG60 HUMAN	O9ug60 homo sapien
20	717.5	59.4	236	2 O4SAL4 TETNG	O4sal4 tetraodon n
21	613.5	50.8	182	2 O5QPQ2 HUMAN	O5qp02 homo sapien
22	608.5	50.4	184	2 O5QPQ0 HUMAN	O5qp00 homo sapien
23	596	49.3	216	2 O917R0 DROME	O917r0 drosophila
24	592.5	49.0	180	2 O5QPQ3 HUMAN	O5qp03 homo sapien
25	558.5	46.2	162	2 O5QPQ1 HUMAN	O5qp01 homo sapien
26	552	45.7	215	2 O7PZW9 ANOGA	O7pzw9 anopheles g
27	552	45.7	216	2 O5TKK0 ANOGA	O5tkk0 anopheles g
28	510.5	42.3	223	2 Q21224 CAEEL	Q21224 caenorhabdi
29	507.5	42.0	239	2 O18501 SCHWA	O18501 schistosoma
30	502.5	41.6	227	2 O9UBF2 SCHJA	O9ubf2 schistosoma
31	495.5	41.0	213	2 O68GW8 CAEEL	O68gw8 caenorhabdi

RESULT 1									
LYPAL HUMAN									
ID	LYPAL HUMAN	STANDARD;							
AC	O75608; O43202; O9UQF9;								
DT	29-MAR-2004 (Rel. 43, Created)								
DT	29-MAR-2004 (Rel. 43, Last sequence update)								
DT	13-SEP-2005 (Rel. 48, Last annotation update)								
DE	Acyl-protein thioesterase 1 (EC 3.1.2.-) (Lysophospholipase I).								
GN	Name=LYPLAI; Synonym=AAPT1, LPL1;								
OS	Homo sapiens (Human)								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;								
OC	Homo.								
OX	NCBI_TaxID=9606;								
[1]									
RN	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).								
RP	Hu G.;								
RA	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.								
RL									
RN	NUCLEOTIDE SEQUENCE (ISOFORM 1), AND X-RAY CRYSTALLOGRAPHY (1.5								
RP	ANGSTROMS) OF 6-230.								
RC	TISSUE=Testis;								
RX	MEDLINE=20535036; PubMed=11080636; DOI=10.1016/S0969-2126(00)00529-3;								
RA	Devedjiev Y., Dauter Z., Kuznetsov S.R., Jones T.L.Z., Derewenda Z.S.;								
RT	"Crystal structure of the human acyl protein thioesterase I from a								
RL	single X-ray data set to 1.5 A.;"								
Structure	8:1137-1146(2000).								
[3]									
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).								
RP	TISSUE=Umbilical cord blood;								
RC	MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;								
RA	Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,								
Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,									
Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,									
"Cloning and functional analysis of cDNAs with open reading frames for									
300 previously undefined genes expressed in CD34+ hematopoietic									
stem/progenitor cells.;"									
RL	Genome Res. 10:1546-1560(2000).								
[4]									
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).								
RP	TISSUE=Bone marrow, and Eye;								
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;								
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,								
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,								
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,								
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,									
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,									
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,									
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,									
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,									
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,									
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,									
Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,									

O4pid3 ustilago ma
Q4isq4 gibberella
Q9hfj5 neurospora
O55qw3 cryptococcu
O5kfa4 cryptococcu
O75gp1 magnaporthe
O51lt0 magnaporthe
O75qp0 magnaporthe
Q6in31 caenorhabdi
Q6bs88 debaryomyce
O83ac9 coxiella bu
O5as12 aspergillus
O6cgl4 yarrowia li
O54t49 dictyosteli

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 127-230 (ISOFORM 1).
RC TISSUE=Brain;
RP Yu W., Sarginson J., Gibbs R.A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Hydrolyzes fatty acids from S-acylated cysteine residues
CC in proteins such as trimeric G alpha proteins or HRAS. Also has
CC low lysophospholipase activity.
CC -!- CATALYTIC ACTIVITY: Palmitoyl-protein + H(2)O = palmitate +
CC protein.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O75608-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O75608-2; Sequence=VSP_009196;
CC Notes=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the AB hydrolase 2 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: AF081281; AAC31610.1; -; mRNA.
DR EMBL: AF291053; AAG10063.1; -; mRNA.
DR EMBL: AF077198; RAD26993.1; -; mRNA.
DR EMBL: AF077199; RAD26994.1; -; mRNA.
DR EMBL: BC008652; AAH08652.1; -; mRNA.
DR EMBL: BC010397; AAH10397.1; -; mRNA.
DR EMBL: AF035293; AAB88180.1; ALT_INIT; mRNA.
DR PDB: 1FJ2; X-ray; A/B=6-230.
DR OGP: O75608; -;
DR PMMA-2DPAGE; O75608; -;
DR Ensembl: ENSG00000120992; Homo sapiens.
DR HGNC: HGNC:6737; LYPLAL1.
DR H-InvDB: HIX0007507; -;
DR MIM: 605599; -;
DR GO: GO:004622; F.lysophospholipase activity; TAS.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF02230; Abhydrolase_2; 1.
DR 3D-structure; Alternative splicing; Fatty acid metabolism; Hydrolase;
KW Lipid metabolism.
FT ACT_SITE 119 119
FT ACT_SITE 174 174
FT ACT_SITE 208 208
FT VARSPPLIC 57 72 Missing (in isoform 2).
FT
FT CONFLICT 127 131 YTALT -> SLIRG (in Ref. 5).
FT
FT SEQUENCE 230 AA; 24670 MW; 90C0522F765F1AC6 CRC64;
SQ
Query Match 99.7%; Score 1204; DB 1; Length 230;
Best Local Similarity 99.6%; Pred. No. 6e-102;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVVP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVVP 60
QY 61 VTLLNNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSIYALTATTOOKLAGVTALSCWLPPLRASLPQGGPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSIYALTATTOOKLAGVTALSCWLPPLRASLPQGGPIGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTILNPNANVTFTKEGMMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTILNPNANVTFTKEGMMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 2

Q6IAQ1 HUMAN
ID Q6IAQ1 HUMAN PRELIMINARY; PRT; 230 AA.
AC Q6IAQ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LYPLAL1 protein.
GN Name=LYPLAL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL: CR457103; CAG33384.1; -; mRNA.
DR SMR: Q6IAQ1; 6-229.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam: PF02230; Abhydrolase_2; 1.
DR Fatty acid metabolism; Lipid metabolism.
KW SEQUENCE 230 AA; 24670 MW; 90C0522F765F1AC6 CRC64;
SQ

Query Match 99.7%; Score 1204; DB 2; Length 230;
Best Local Similarity 99.6%; Pred. No. 6e-102;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVVP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVVP 60
QY 61 VTLLNNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSIYALTATTOOKLAGVTALSCWLPPLRASLPQGGPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSIYALTATTOOKLAGVTALSCWLPPLRASLPQGGPIGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTILNPNANVTFTKEGMMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTILNPNANVTFTKEGMMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 3

Q5RBR7 PONPY
ID Q5RBR7 PONPY PRELIMINARY; PRT; 230 AA.
AC Q5RBR7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459O0134.
GN Name=DKFZp459O0134;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OC NCBI_TaxID=9600;
RN

use as long as its content is in no way modified and this statement is not removed.

CC -----
 CC EMBL; U9352; AAB48627.1; -; mRNA.
 DR EMBL; AK002674; BAB22276.1; -; mRNA.
 DR EMBL; AK005049; BAC34318.1; ALT INIT; mRNA.
 DR EMBL; BC013536; AAH13536.1; -; mRNA.
 DR EMBL; BC052848; AAH52848.1; -; mRNA.
 DR HSSP; O75608; 1FJ2.
 DR SMR; P97823; 6-229.
 DR Ensembl; ENSMUSG00000025903; Mus musculus.
 DR MGI; MGI:1344588; Lyp1a1.
 DR GO; GO:0005739; C:mitochondrion; IDA.
 DR InterPro; IPR003140; PLP Cesterase.
 DR InterPro; IPR000379; Ser-estrs.
 DR Pfam; PF02230; Abhydrolase_2; 1.
 DR Alternative splicing; Direct protein sequencing;
 KW Fatty acid metabolism; Hydrolase; Lipid metabolism.
 FT ACT SITE 119 119
 FT ACT SITE 174 174
 FT ACT SITE 208 208
 FT VARSPLIC 214 230
 FT EMDVKHFIDKLLPPID -> VGVSGSSE (in isoform 2).

FT /FTid=VSP 009197.
 FT S->A: Abolishes lysophospholipase
 FT activity.
 FT D->A: Abolishes lysophospholipase
 FT activity.
 FT H->A: Abolishes lysophospholipase
 FT activity.
 FT P -> L (in Ref. 3; AAH52848) .
 FT CONFLICT 156 156
 FT ACT SITE 174 174
 FT ACT SITE 208 208
 FT ACT SITE 214 230
 FT EMDVKHFIDKLLPPID -> VGVSGSSE (in isoform 2).

Query Match 93.5%; Score 1130; DB 1; Length 230;
 Best Local Similarity 91.3%; Pred. No. 3.7e-95;
 Matches 210; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 QY 61 VTLLNNVAMPSPFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VTLLNNVAMPSPFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 121 GGALSITYALTITTOQKLAGVTALSCWLPPLRASLPQGPICGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSITYALTITTOQKLAGVTALSCWLPPLRASLPQGPICGANRDISILOCHGDCDPLVPLM 180
 QY 181 FGSLTVEKLTIVNPANVTFTKTYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
 DB 181 FGSLTVERLKALINPANVTFTKTYEGNMHSSCOQEMMDVKHFDKLLPPID 230

RESULT 5
 LYPAL RABIT
 ID LYPAL RABIT STANDARD; PRT; 230 AA.
 AC O77821;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl-protein thioesterase 1 (EC 3.1.2.-) (Lysophospholipase I)
 DE (Calcium-independent phospholipase A2) (CaPLA2).
 DE Name=Lyp1a1;
 GN Oryctolagus cuniculus (Rabbit).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 98-103; 150-161 AND
 RP 191-201.
 RC TISSUE=Kidney;

RX MEDLINE=98308497; PubMed=9644627;
 RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
 RA Sasser M., Cheng J., Buonanno A.;
 RT "cDNA cloning and expression of a novel family of enzymes with
 RT calcium-independent phospholipase A2 and lysophospholipase
 RT activities.";
 RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
 CC -!- FUNCTION: Hydrolizes fatty acids from S-acylated cysteine residues
 CC in proteins such as trimeric G alpha proteins or HRAS. Also has
 CC low lysophospholipase activity (By similarity).
 CC -!- CATALYTIC ACTIVITY: Palmitoyl-protein + H(2)O = palmitate +
 CC protein.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the AB hydrolase 2 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; U97148; AAC63432.1; -; mRNA.
 DR HSSP; O75608; 1FJ2.
 DR SMR; O77821; 6-229.
 DR InterPro; IPR003140; PLP Cesterase.
 DR InterPro; IPR000379; Ser-estrs.
 DR Pfam; PF02230; Abhydrolase_2; 1.
 KW Direct protein sequencing; Fatty acid metabolism; Hydrolase;
 KW Lipid metabolism.
 FT ACT SITE 119 119 By similarity.
 FT ACT SITE 174 174 By similarity.
 FT ACT SITE 208 208 By similarity.
 FT ACT SITE 214 230 By similarity.
 FT SEQUENCE 230 AA; 24688 MW; 89AF2017AEFC9FAC CRC64;

Query Match 93.5%; Score 1130; DB 1; Length 230;
 Best Local Similarity 91.3%; Pred. No. 3.7e-95;
 Matches 210; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
 QY 61 VTLLNNVAMPSPFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VTLLNNVAMPSPFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 121 GGALSITYALTITTOQKLAGVTALSCWLPPLRASLPQGPICGANRDISILOCHGDCDPLVPLM 180
 DB 121 GGALSITYALTITTOQKLAGVTALSCWLPPLRASLPQGPICGANRDISILOCHGDCDPLVPLM 180
 QY 181 FGSLTVEKLTIVNPANVTFTKTYEGNMHSSCOQEMMDVKQFIDKLLPPID 230
 DB 181 FGSLTVERLKALINPANVTFTKTYEGNMHSSCOQEMMDVKHFDKLLPPID 230

RESULT 6
 Q4FK51 MOUSE
 ID Q4FK51_MOUSE PRELIMINARY; PRT; 230 AA.
 AC Q4FK51;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Lyp1a1 protein.
 GN Name=Lyp1a1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
 RA Mollenhauer J., Wiemann S., Schick M., Korn B.;

RT "Cloning of mouse full open reading frames in Gateway(R) system entry
RT vector [pDONR201].";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; C7010201; CAJ18409.1; -; mRNA.
SQ SEQUENCE 230 AA; 24689 MW; 0387829D8656BFA2 CRC64;

Query Match 93.2%; Score 1126; DB 2; Length 230;
Best Local Similarity 90.9%; Pred. No. 8.6e-95;
Matches 209; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARATATAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARATATAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLLNMVAMPSPFDIIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNMVAMPSPFDIIIGLSPDSQEDSGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSLYLTALTTOQKLAGVTALSCWLPRLASFPQGPFGINSANRDISVLQCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKYEYGMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVERLKLALNPANVTFTKYEYGMHSSCCQEMMDVKHFIDKLLPPID 230

RESULT 7
ID LYPAL_RAT STANDARD; PRT; 230 AA.
AC P70470;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl-protein thioesterase 1 (EC 3.1.2.-) (lysophospholipase I).
GN Names=Lyplal; Synonyms=Aptl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 20-30 AND 192-196, FUNCTION,
RP AND TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=96205961; PubMed=8631810; DOI=10.1074/jbc.271.13.7705;
RA Sugimoto H., Hayashi H., Yamashita S.;
RT "Purification, cDNA cloning, and regulation of lysophospholipase from
RT rat liver";
RN J. Biol. Chem. 271:7705-7711(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE, FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Hypothalamus;
RX MEDLINE=98308497; PubMed=9644627;
RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
RA Sasner M., Cheng J., Buonanno A.;
RT "cDNA cloning and expression of a novel family of enzymes with
RT calcium-independent phospholipase A2 and lysophospholipase
RT activities";
RN J. Am. Soc. Nephrol. 9:1178-1186(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Heart;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PROTEIN SEQUENCE OF 98-112 AND 191-201, AND FUNCTION.
RX PubMed=9624183; DOI=10.1074/jbc.273.25.15830;
RA Duncan J.A., Gilman A.G.;
RT "A cytoplasmic acyl-protein thioesterase that removes palmitate from G
RT protein alpha subunits and p21(RAS).";
RL J. Biol. Chem. 273:15830-15837(1998).
CC -I- FUNCTION: Hydrolyzes fatty acids from S-acylated cysteine residues

CC in proteins such as trimeric G alpha proteins or HRAS. Also has
CC low lysophospholipase activity.
CC -I- CATALYTIC ACTIVITY: Palmitoyl-protein + H(2)O = palmitate +
CC protein.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- TISSUE SPECIFICITY: Ubiquitous. Detected at low levels in all
CC tissues tested.
CC -I- SIMILARITY: Belongs to the AB hydrolase 2 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; D63885; BAA09935.1; -; mRNA.
DR EMBL; U97146; AAC63430.1; -; mRNA.
DR EMBL; BC085750; AAH85750.1; -; mRNA.
DR HSSP; O75608; 1FJ2.
DR SMR; P70470; 6-229.
DR Ensembl; ENSRNOG00000008320; Rattus norvegicus.
DR GO; GO:0004622; F:lysophospholipase activity; IDA.
DR InterPro; IPR003140; PLP Cesterase.
DR InterPro; IPR000379; Ser-estrs.
DR Pfam; PF02230; Abhydrolase_2; 1.
DR Direct protein sequencing; Fatty acid metabolism; Hydrolase;
KW Lipid metabolism.
FT ACT_SITE 119 119 By similarity.
FT ACT_SITE 174 174 By similarity.
FT ACT_SITE 208 208 By similarity.
SQ SEQUENCE 230 AA; 24709 MW; AAPE8C4702EAD74 CRC64;

Query Match 93.1%; Score 1125; DB 1; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.1e-94;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARATATAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARATATAVIFLHGLGDTGHWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLLNMVAMPSPFDIIIGLSPDSQEDSGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLLNMVAMPSPFDIIIGLSPDSQEDSGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSLYLTALTTOQKLAGVTALSCWLPRLASFPQGPFGINSANRDISVLQCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKYEYGMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVERLKLALNPANVTFTKYEYGMHSSCCQEMMDVKFIDKLLPPID 230

RESULT 8
ID 077820_RABIT PRELIMINARY; PRT; 219 AA.
AC 077820;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium-independent phospholipase A2 isoform 1 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=98308497; PubMed=9644627;
RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
RA Sasner M., Cheng J., Buonanno A.;
RT "cDNA cloning and expression of a novel family of enzymes with

RT calcium-independent phospholipase A2 and lysophospholipase
 RT activities.";
 RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
 DR EMBL; U97147; AAC63431.1; -, mRNA.
 DR HSSP; O75608; 1FJ2.
 DR SMR; O77820; 1-218.

DR GO; GO:0003824; F:catalytic activity; IEA.
 DR InterPro; IPR003140; PLP_Cesterase.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF02230; Abhydrolase_2; 1.
 FT NON_TER 1

SQ SEQUENCE 219 AA; 23602 MW; 3B6A4FEDC3BC912B CRC64;

Query Match 91.5%; Score 1105; DB 2; Length 219;

Best Local Similarity 96.3%; Pred. No. 6.8e-93;

Matches 211; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 12 AIVPAARKATAAVIFLHGLGDTGHGWAEPAGIRSHIKYICHPAPVRPVTLLNMVAMPS 71

Db 1 ASVPAARKATAAVIFLHGLGDTGHGWAEPAGIRSHIKYICHPAPVRPVTLLNMVAMPS 60

QY 72 WFDIIGLSPDSQDESGIQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSILYALT 131

Db 61 WFDIIGLSPDSQDESGIQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSILYALT 120

QY 132 TQOKLAGVTALSCWPLRASLPQGPIGGANRDISILQCHGDCDPLVPLMFGSLTVEKLT 191

Db 121 TQOKLAEVTALSCWPLRASLPQGPISGANRDISILQCHGDCDPLVPLMFGSLTVEKLT 180

QY 192 LVNPANVTFTYEGMMHSSCQEQEMDMVKQFIDKLLPPID 230

Db 181 LVNPANVTFTYEGMMHSSCQEQEMDMVKQFIDKLLPPID 219

RESULT 9

Q6DJB2 XENTR

ID Q6DJB2_XENTR PRELIMINARY; PRT; 230 AA.

AC Q6DJB2_

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Lysophospholipase II.

GN Names=lypla2-prov;

OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus; Silurana.

OX NCBI_TaxID=8364;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole body;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole body;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

Q6GP07 XENLA

ID Q6GP07_XENLA PRELIMINARY; PRT; 230 AA.

AC Q6GP07_

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE MGC80756 protein.

GN Name=MGC80756;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

Q6GP07 XENLA

ID Q6GP07_XENLA PRELIMINARY; PRT; 230 AA.

AC Q6GP07_

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE MGC80756 protein.

GN Name=MGC80756;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RC NUCLEOTIDE SEQUENCE.
 RP TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CR EMBL; BC073342; AAH73342.1; -; mRNA.
 DR SMR; Q6GP07; 6-229.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0006631; P:fatty acid metabolism; IEA.
 DR GO; GO:0006629; P:lipid acid metabolism; IEA.
 DR InterPro; IPR003140; PLP_Cesterase.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF02230; Abhydrolase_2; 1.
 KW Fatty acid metabolism; Hydrolase; Lipid metabolism.
 SQ SEQUENCE 230 AA; 24454 MW; ABE5E723B896DB69 CRC64;

Query Match 84.9%; Score 1025; DB 2; Length 230;
 Best Local Similarity 80.4%; Pred. No. 1.6e-85;
 Matches 185; Conservative 24; Mismatches 21; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPATVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
 DB 1 MCGNTWSALPALVPAARKATAAIVFLHGLGDTGHWAEAMASIKSPHVYKICPHAPIMP 60
 QY 61 VTLLNMVAMPSWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VSLNMNMAMPSWFDIIGLSPDAEDEAGIKKAENVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 121 GGALSYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGGANRDISILQCHGCDPLVPLM 180
 DB 121 GGALSYLTALTTOQKLGGVVVALSCWLPRLRSFPQAAANSANKDVAVLQCHGESDPLVPLM 180
 QY 181 FGSLTVEKLTIVNPANVTFTYEGMMHSSCOQENMDVKQFDKLPPI 230
 DB 181 FGTITSEKLTIIIPANVFKTYGLMHSNCOEMTDIKQFDKQLPPVN 230

RESULT 11
 QARN09_TETNG PRELIMINARY; PRT; 229 AA.
 AC QARN09;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 6 SCAF15017, whole genome shotgun sequence.
 DE (Fragment).
 DE ORFNames=GSTENG00031789001;
 GN Tetraodon nigroviridis (Green puffer).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudat V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype";
 RL Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CR EMBL; CAAB01015017; CAG10223.1; -; Genomic_DNA.
 FT NON_TER 229
 SQ SEQUENCE 229 AA; 24798 MW; 7976729B2D7683AA CRC64;

Query Match 78.6%; Score 950; DB 2; Length 229;
 Best Local Similarity 74.2%; Pred. No. 1.2e-78;
 Matches 170; Conservative 32; Mismatches 27; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
 DB 1 MCGNSMSPALPAIVPAARRATAAIVFLHGLGDTGHSWADFAGLRUPHVKYICPHAPVMP 60
 QY 61 VTLLNMVAMPSWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 DB 61 VSLNMNMAMPSWFDIIGLSPDAEDEPGIKQAENIKAMIDQEVKNGIPSHRIILGGFSQ 120
 QY 121 GGALSYLTALTTOQKLAGVTALSCWLPRLASLPQGPFGGANRDISILQCHGCDPLVPLM 180
 DB 121 GGALSYLTALTTOQKLAGVVVALSCWLPRLKSPQASANSANKDLHLVQCHGADPVPFV 180
 QY 181 FGSLTVEKLTIVNPANVTFTYEGMMHSSCOQENMDVKQFDKLPPI 229
 DB 181 FGTQTAERKMSLVNPSHMSFKTYRGLCHSACPPEEMVDIKRFEKQLPPL 229

RESULT 12
 Q6PBW8_BRARE PRELIMINARY; PRT; 232 AA.
 AC Q6PBW8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein zgc:73210;
 GN ORFNames=zgc:73210;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=wild-type; TISSUE=EYE;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Wild-type; TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 DR EMBL; BC059556; AAH59556.1; --; mRNA.
 DR HSSP; Q53547; 1AUO.
 DR ZFIN; ZDB-GENE-040426-1715; zgc:73210.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0008631; P:fatty acid metabolism; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR InterPro; IPR003140; PLP Cesterase.
 DR InterPro; IPR000379; Ser_estr.
 DR Pfam; PF02230; Abhydrolase_2; 1.
 DR Fatty acid metabolism; Hydrolase; Hypothetical protein;
 KW Lipid metabolism.
 SQ SEQUENCE 232 AA; 25067 MW; 03519A06130EA550 CRC64;

Query Match 71.7%; Score 866.5; DB 2; Length 232;
 Best Local Similarity 68.5%; Pred. No. 5.3e-71;
 Matches 159; Conservative 28; Mismatches 42; Indels 3; Gaps 1;

QY 1 MCGNNMSTPLP---TVPAAKATAAIVFLHGLGDTGHGWAFAFAGIRSHIKYICPHAP 57
 DB 1 MCGNNMSTPLPAAEAVTPGTEKETAIVFLHGLGDTGHGWADAMTSIRLPYIKYICPHAP 60
 QY 58 VRPVTLMNVMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGG 117
 DB 61 RIPVTLLNKMVPSWFDLMLGLSPDEDEAGIKKAAENIKALIDHEVKNGIPSNRIILGG 120
 QY 118 FSQGGALSILYALTTOQKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLV 177
 DB 121 FSQGGALSILYALTSTOQKLAGVVGSLCWLPLHKTFPQAGASANKDTPILQCHGMDPMI 180
 QY 178 PLMFGSLTVKELKTLVNPANVTFTKYEYGMHSSCOQEMDMVKQFIDKLPLPI 229
 DB 181 PVQFGAMTAELKLTIVSPENITFTPTPLGMHSSCPQEMSAAVKDFIEKQLPRV 232

RESULT 13
 LYP2 RAT
 ID LYP2 RAT STANDARD; PRT; 231 AA.
 AC Q9QVL6;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl-protein thioesterase 2 (EC 3.1.2.-) (Lysophospholipase II)
 DE (Lysophospholipase 2).
 GN Name=Lyp1a2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sugimoto H.;
 RT "Rat lysophospholipase II.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung;
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May hydrolyze fatty acids from S-acylated cysteine
 residues in proteins such as trimeric G alpha proteins or HRAS (By

CC similarity). Has lysophospholipase activity (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -!- SIMILARITY: Belongs to the AB hydrolase 2 family.
 CC -----
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; AB021645; BAA87911.1; --; mRNA.
 DR EMBL; BC070503; AAH70503.1; --; mRNA.
 DR HSSP; O75608; 1FJ2.
 DR Ensembl; ENSRNOG00000010067; Rattus norvegicus.
 DR InterPro; IPR003140; PLP Cesterase.
 DR InterPro; IPR000379; Ser_estr.
 DR Pfam; PF02230; Abhydrolase_2; 1.
 KW Fatty acid metabolism; Hydrolase; Lipid metabolism.
 FT ACT SITE 122 122 By similarity.
 FT ACT SITE 176 176 By similarity.
 FT ACT SITE 210 210 By similarity.
 SQ SEQUENCE 231 AA; 24807 MW; 49A710C5A997C7C1 CRC64;

Query Match 70.4%; Score 851; DB 1; Length 231;
 Best Local Similarity 68.1%; Pred. No. 1.4e-69;
 Matches 158; Conservative 30; Mismatches 40; Indels 4; Gaps 2;

QY 1 MCGNNMSTPL---PAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSHIKYICPHAP 57
 DB 1 MCGNNMSTPLLDATAATVSGAERETAIVFLHGLGDTGHGWADALSTIRLPYIKYICPHAP 60
 QY 58 VRPVTLMNVMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGG 117
 DB 61 RIPVTLLNKMVPSWFDLMLGLSPDEDEAGIKKAAENIKALIDHEVKNGIPSNRIILGG 120
 QY 118 FSQGGALSILYALTTOQKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLV 177
 DB 121 FSQGGALSILYALTALCPHPLAGIVALSCWLPPLHRNFPQAANGSA-KDLAILQCHGELDPV 179
 QY 178 PLMFGSLTVKELKTLVNPANVTFTKYEYGMHSSCOQEMDMVKQFIDKLPLPI 229
 DB 180 PVRFGALTAEKLTURVTVPARVQKTPGVGMHSSCPQEMAIVKFELEKLPVP 231

RESULT 14
 LYP2 MOUSE
 ID LYP2 MOUSE STANDARD; PRT; 231 AA.
 AC Q9WTL7;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl-protein thioesterase 2 (EC 3.1.2.-) (Lysophospholipase II)
 DE (Lysophospholipase 2) (Mlyso II).
 GN Name=Lyp1a2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=99165589; PubMed=10064901; DOI=10.1016/S1388-1981(99)00007-4;
 RA Toyoda T., Sugimoto H., Yamashita S.;
 RT "Sequence, expression in Escherichia coli, and characterization of
 lysophospholipase II.";
 RL Biochim. Biophys. Acta 1437:182-193 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Embryo, Kidney, and Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Glissi C., Godzik A., Gough J., Grimmond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G., Petrovsky N., Pillai R., Pontius J.O., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs." Nature 420:563-573 (2002). [3]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: May hydrolyze fatty acids from S-acylated cysteine residues in proteins such as trimeric G alpha proteins or HRAS (By similarity). Has lysophospholipase activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- TISSUE SPECIFICITY: Ubiquitous; detected at low levels.
 CC -1- SIMILARITY: Belongs to the AB hydrolase 2 family.
 CC -----
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 CC -----
 CC EMBL; AB009653; BAA76751.1; -; mRNA.
 CC EMBL; AK003689; BAB22940.1; -; mRNA.
 CC EMBL; AK075590; BAC35841.1; -; mRNA.
 CC EMBL; AK089112; BAC40757.1; -; mRNA.
 CC EMBL; BC068120; AAK68120.1; -; mRNA.
 CC HSP; O75608; 1FJ2.
 CC ENSembl; ENSMUSG00000028670; Mus musculus.
 CC MGI; MGI:1347000; Lypla2.
 CC InterPro; IPR003140; PLP_Cesterase.

DR InterPro; IPR000379; Sex_estrs.
 KW Pfam; PF02230; Abhydrolase_2; 1.
 KW Fatty acid metabolism; Hydrolase; Lipid metabolism.
 FT ACT_SITE 122 122 By similarity.
 FT ACT_SITE 176 176 By similarity.
 FT ACT_SITE 210 210 By similarity.
 SQ SEQUENCE 231 AA; 24794 MW; E18797A17570AA97 CRC64;
 Query Match 70.0%; Score 845; DB 1; Length 231;
 Best Local Similarity 67.7%; Pred. No. 4.9e-69;
 Matches 157; Conservative 30; Mismatches 41; Indels 4; Gaps 2;
 QY 1 MCGNNMSTPL---PAIVPAARKATRAVIFLHGLDTHGHWAEAFAGIRSHIKYICPHAP 57
 DB 1 MCGNTMSVPLLTDAATVSGAERETAIVIFLHGLDTHGHWADALSTIRLPHVYIICPHAP 60
 QY 58 VRPVTILNMVAMPSPFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGG 117
 DB 61 RIVPTILNMVAMPSPFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGG 120
 QY 118 FSQGGALSLYTALTTOOKLAGVTALSCWPLRLASLPQGPPIGGANRDISILOCHGDCDPLV 177
 DB 121 FSQGGALSLYTALTTCPLPLAGIVALSCLPLHRNFPQAAANGSA-KDLAILQCHGELDPMV 179
 QY 178 PLMFGLSLTYEKLTLVNPANVTFTYEGVHSSCOQEMDMVKQFIDKLPPPI 229
 DB 180 PVRFGALTAEKLRVTVPARVQFKTPYGVHSSCPQEMAQVKEFLEKLUPPV 231

RESULT 15
 LYP2 HUMAN
 ID LYP2 HUMAN STANDARD; PRT; 231 AA.
 AC 095372; Q724Z2;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl-protein thioesterase 2 (EC 3.1.2.-) (Lysophospholipase II) (LPL-1).
 GN Names=LYPLA2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Testis;
 KU Kuznetsov S.R., Jones T.L.Z.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RG Human chromosome 1 international sequencing consortium;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RU Yue P., Yu L., Tu Q., Ding J.B., Fu S.N., Zhao S.Y.;
 RT "Cloning and expression of a novel human cDNA homology to murine lysophospholipase I mRNA." Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC Tissue=Colon, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Yung A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May hydrolyze fatty acids from S-acylated cysteine
residues in proteins such as trimeric G alpha proteins or HRAS.
CC Has lysophospholipase activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the AB hydrolase 2 family.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
in positions 5, 164 and 179.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

CC EMBL; AF098668; AAC72844.1; -; mRNA.
DR EMBL; AL031295; CAB40158.1; -; Genomic DNA.
DR EMBL; AF098423; AAP97210.1; ALT_FRAME; mRNA.
DR EMBL; BC017034; AAH17034.1; -; mRNA.
DR EMBL; BC017193; AAH17193.1; -; mRNA.
DR HSSP; O75608; 1FJ2.
DR OGP; O95372; -.
DR Ensembl; ENSG00000011009; Homo sapiens.
DR HGNC; HGNC:6738; LYPLA2.
DR H-InvDB; HIX0000255; -.
DR InterPro; IPR003140; PLP_Cesterase.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF02230; Abhydrolase 2; 1.
KW Fatty acid metabolism; Hydrolase; Lipid metabolism.
FT ACT_SITE 122 122 By similarity.
FT ACT_SITE 176 176 By similarity.
FT ACT_SITE 210 210 By similarity.
SQ SEQUENCE 231 AA; 24737 MW; 813C9C71757C5135 CRC64;

Query Match 69.6%; Score 841; DB 1; Length 231;
Best Local Similarity 67.2%; Pred. No. 1.2e-68;
Matches 156; Conservative 31; Mismatches 41; Indels 4; Gaps 2;

QY 1 MCGNNMSTPL---PAIVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSHIKYICPHAP 57
DB 1 MCGNTMSVPLLTDAATVSGAERETAAVIFLHGLGDTGHSWADALSTIRLPHVKYICPHAP 60

QY 58 VRPVTLMNVMPSWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGG 117
DB 61 RIPVTLMNKMVPSWFDLMGLSPDAPEDBAGIKKAAENIKALIEHEMKNGIPANRIVLGG 120

QY 118 FSQGGALSUYALTTOQKLAGVTALSCWPLPLRASLPQGPIGGANRDISILQCHGDCDPLV 177
DB 121 FSQGGALSUYALTCPHPLAGIVALSCLWPLHRAFPQAAANGSA-KDLAILQCHGELDPV 179

QY 178 PLMFGSLITVEKLTLPNPNVTFKTEGMHSSCQEQEMDMVKQIDKLLPPI 229
DB 180 PVRFGALTAEKLSRVVTPARVQKTYFGVMHSSCPQEMAQVKEFLEKLLPPV 231

Search completed: April 13, 2006, 21:17:55
Job time : 236 secs

QY 61 VTLMNVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 VTLMNVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSlyTALTtTQOKLAGVTALSCWLPPLRASLPQGGIGGANRDISILOCHGDCDPLVPLM 180
Db 121 GGALSlyTALTtTQOKLAGVTALSCWLPPLRASLPQGGIGGANRDISILOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTlVNPANVTfKTYEGMHSSCOQEMMDVKQFIDKLLPPID 230
Db 181 FGSLTVEKLTlVNPANVTfKTYEGMHSSCOQEMMDVKQFIDKLLPPID 230

RESULT 2

US-09-216-386-3
; Sequence 3, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-216-386-3

Query Match 99.7%; Score 1204; DB 2; Length 230;
Best Local Similarity 99.6%; Pred. No. 1.4e-127;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHCWAEAFAGIRSSHIIKYICHPAPVRP 60
Db 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHCWAEAFAGIRSSHIIKYICHPAPVRP 60
QY 61 VTLMNVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 VTLMNVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSlyTALTtTQOKLAGVTALSCWLPPLRASLPQGGIGGANRDISILOCHGDCDPLVPLM 180
Db 121 GGALSlyTALTtTQOKLAGVTALSCWLPPLRASLPQGGIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTlVNPANVTfKTYEGMHSSCOQEMMDVKQFIDKLLPPID 230
Db 181 FGSLTVEKLTlVNPANVTfKTYEGMHSSCOQEMMDVKQFIDKLLPPID 230

RESULT 3

US-08-844-120-3
; Sequence 3, Application US/08844120
; Patent No. 5858756
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 552244
US-08-844-120-3

Query Match 93.1%; Score 1125; DB 1; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHCWAEAFAGIRSSHIIKYICHPAPVRP 60
Db 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHCWAEAFAGIRSSHIIKYICHPAPVRP 60
QY 61 VTLMNVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 VTLMNVAMPSWFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSlyTALTtTQOKLAGVTALSCWLPPLRASLPQGGIGGANRDISILOCHGDCDPLVPLM 180
Db 121 GGALSlyTALTtTQOKLAGVTALSCWLPPLRASLPQGGIPSNRDISVLQCHGDCDPLVPLM 180
QY 181 FGSLTVEKLTlVNPANVTfKTYEGMHSSCOQEMMDVKQFIDKLLPPID 230
Db 181 FGSLTVEKLTlVNPANVTfKTYEGMHSSCOQEMMDVKYFIDKLLPPID 230

RESULT 4

US-09-022-940-5
; Sequence 5, Application US/09022940
; Patent No. 5965423

```

;
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,862
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1552244
; US-09-022-940-5

Query Match 93.1%; Score 1125; DB 1; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSYLTALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSYLTALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKYEYGMHSSCOQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLKTLVNPANVTFTKYEYGMHSSCOQEMMDVKQFIDKLLPPID 230

RESULT 5
US-09-216-001-3
; Sequence 3, Application US/09216001
; Patent No. 6004792
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

;
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,862
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0329 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1552244
; US-09-216-001-3

Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAEAFAGIRSHIKYICHPAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAEAFAGIRSHIKYICHPAPVRP 60
QY 61 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSYLTALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180
DB 121 GGALSYLTALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILQCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKYEYGMHSSCOQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLKTLVNPANVTFTKYEYGMHSSCOQEMMDVKQFIDKLLPPID 230

RESULT 6
US-09-216-386-5
; Sequence 5, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
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; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-216-386-5

Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0

QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTDGHGWAEPAGIRSSHIIKVICPHAPVRP 60
Db 1 MCGNNMSAPWPAVPAARKATAAVIFLHGLGDTDGHGWAEPAGIKSHIKVICPHAPVMP 60
QY 61 VTLMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 VTLMNMMPSWFDIIGLSPDSQDESGIKQAETVTKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOQKLAGVTALS CWLPLRASLPQGPITGGANRDISILQCHGDCDPLVPLM 180
Db 121 GGALSLYTALTTOQKLAGVTALS CWLPLRASFSQGPINSANRDISVLQCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTYEGMMHSSCQEQEMDMVKQFIDKLLPPID 230
Db 181 FGSLTVERLKGVLNPANVTFAVYEGMMHSSCQEQEMDMVKYFIDKLLPPID 230

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1  RESULT 7
2  US-08-878-862-3
3  ; Sequence 3, Application US/08878862
4  ; Patent No. 6143544
5  ;
6  ; GENERAL INFORMATION:
7  ; APPLICANT: Hillman, Jennifer L.
8  ; APPLICANT: Shah, Purvi
9  ; APPLICANT: Corley, Neil C.
10 ; APPLICANT: Murry, Lynn E.
11 ;
12 ; TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
13 ;
14 ; NUMBER OF SEQUENCES: 4
15 ;
16 ; CORRESPONDENCE ADDRESS:
17 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
18 ; STREET: 3174 Porter Drive
19 ; CITY: Palo Alto
20 ; STATE: CA
21 ;
22 ; COUNTRY: USA
23 ; ZIP: 94304
24 ;
25 ; COMPUTER READABLE FORM:
26 ; MEDIUM TYPE: Diskette
27 ; COMPUTER: IBM Compatible
28 ; OPERATING SYSTEM: DOS
29 ; SOFTWARE: FASTSEQ for Windows Version 2.0
30 ; CURRENT APPLICATION DATA:
31 ; APPLICATION NUMBER: US/08/878,862

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; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0329 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1552244
;
US-08-878-862-3

Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MCGNNMSTPLPAVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSSHSHKVICHPAPVRP 60
Db 1 MCGNNMSAPVAVVPAARKATAAVIFLHGLGDTGHWAEAFAGIKSSHSHKVICHPAPVMP 60
Qy 61 VTLNMNVAMPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 VTLNMSMMESWFDDIIGLSPDSQDESGIKQAETVKALIDQEVKNGIPSNRIILGGFSQ 120
Qy 121 GGALSPLYTALTTOOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
Db 121 GGALSPLYTALTTOOKLAGVTALSCWLPRLASFSQGPINSANRDISVLQCHGDCDPLVPLM 180
Qy 181 FGSLTVEKLTALVNPANVTFKTVEGMHSSCCQEMMDVKOFIDKLLPPID 230
Db 181 FGSLTVERLGLVNPANVTFKVTEGMHSSCCQEMMDVKFIDKLLPPID 230

RESULT 8
US-09-213-394-3
; Sequence 3, Application US/09213394
; Patent No. 6319701
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,394
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE:

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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 552244
US-09-213-394-3

Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNMSAPMPAPVPAARKATAAIVFLHGLGDTGHGWAFAFAGIKSSHIIKYICPHAPVMP 60
QY 61 VTLMNVAMPWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLMNSMMPWFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOQKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTOQKLAGVTALSCWLPPLRASLPQGPINSANRDISVLOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKYEYGMHSSCOQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVERLKLGLVNPANVTFTKYEYGMHSSCOQEMMDVKYFIDKLLPPID 230

RESULT 9
US-09-988-982-3
Sequence 3, Application US/09988982
Patent No. 6838245
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988.982
FILING DATE: 19-NO. 6838245-2001
PRIOR APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELEPHONE: 415-855-0555

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 552244
US-09-988-982-3

Query Match 93.1%; Score 1125; DB 2; Length 230;
Best Local Similarity 91.7%; Pred. No. 1.2e-118;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNMSAPMPAPVPAARKATAAIVFLHGLGDTGHGWAFAFAGIKSSHIIKYICPHAPVMP 60
QY 61 VTLMNVAMPWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTLMNSMMPWFDIIGLSPDSQDESGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
QY 121 GGALSLYTALTTOQKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSLYTALTTOQKLAGVTALSCWLPPLRASLPQGPINSANRDISVLOCHGDCDPLVPLM 180
QY 181 FGSLTVEKLKTLVNPANVTFTKYEYGMHSSCOQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVERLKLGLVNPANVTFTKYEYGMHSSCOQEMMDVKYFIDKLLPPID 230

RESULT 10
US-08-844-120-1
Sequence 1, Application US/08844120
Patent No. 5858756
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: KIDNNOT19
CLONE: 2676650
US-08-844-120-1
Query Match 85.1%; Score 1028; DB 1; Length 208;
Best Local Similarity 88.7%; Pred. No. 9.4e-108;
Matches 204; Conservative 0; Mismatches 4; Indels 22; Gaps 1;
QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTG-----PVRP 38
QY 61 VTLLNNVAMPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 39 VTLLNNVAMPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
QY 121 GGALSLYALTATTOOKLAGVTALSCWLPPLRASIPQGPPIGGANRDISILOCHGDCDPLVPLM 180
Db 99 GGALSLYALTATTOOKLAGVTALSFLLPLRXSPQGPPIGGANRDISILOCHGDCDPLVPLM 158
QY 181 FGSLTVEKLTILVNPANVTFTKTYEGMHSSCOQEMMDVKQFIDKLLPPID 230
Db 159 FGSLTVEKLTILVNPANVTFTKTYEGMHSSCOQEMMDVKQFIDKLLPPID 208

RESULT 11

US-09-213-394-1
Sequence 1, Application US/09213394
Patent No. 6319701
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,394
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNNOT19
CLONE: 2676650
US-09-213-394-1
Query Match 85.1%; Score 1028; DB 2; Length 208;
Best Local Similarity 88.7%; Pred. No. 9.4e-108;

Matches 204; Conservative 0; Mismatches 4; Indels 22; Gaps 1;
QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTG-----PVRP 38
QY 61 VTLLNNVAMPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 39 VTLLNNVAMPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
QY 121 GGALSLYALTATTOOKLAGVTALSCWLPPLRASIPQGPPIGGANRDISILOCHGDCDPLVPLM 180
Db 99 GGALSLYALTATTOOKLAGVTALSFLLPLRXSPQGPPIGGANRDISILOCHGDCDPLVPLM 158
QY 181 FGSLTVEKLTILVNPANVTFTKTYEGMHSSCOQEMMDVKQFIDKLLPPID 230
Db 159 FGSLTVEKLTILVNPANVTFTKTYEGMHSSCOQEMMDVKQFIDKLLPPID 208

RESULT 12

US-09-988-982-1
Sequence 1, Application US/09988982
Patent No. 6838245
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,982
FILING DATE: 19-No. 6838245-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNNOT19
CLONE: 2676650
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-988-982-1

Query Match 85.1%; Score 1028; DB 2; Length 208;
Best Local Similarity 88.7%; Pred. No. 9.4e-108;
Matches 204; Conservative 0; Mismatches 4; Indels 22; Gaps 1;
QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTG-----PVRP 38

[illegible]

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RESULT 13
US-09-022-940-1
; Sequence 1, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,940
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-022-940-1

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181 FGSLTVEKLTLYNPANVTFTKYEGMHSSCQEQEMMDVKQFIDKLLPPI 229
159 FGSLTVEKLTLYNPANVTFTKYEGMHSSCQEQEMMDVKQFIDKLLPPI 207

RESULT 14
US-09-216-386-1
; Sequence 1, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-216-386-1

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RESULT 15
US-09-013-881-7
; Sequence 7, Application US/09013881
; Patent No. 6132964

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 21:29:33 ; Search time 167 Seconds
(without alignments)
575.454 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTPLPAIVPAARKA.....COQEMMDVKQFDKLLPPID 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 segs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA Main:*
- 1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pbp:**
 - 2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pbp:**
 - 3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pbp:**
 - 4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pbp:**
 - 5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pbp:**
 - 6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pbp:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1204	99.7	230	4	US-10-236-417-64
2	1204	99.7	263	3	US-09-925-299-991
3	1204	99.7	263	3	US-09-925-299-991
4	1204	99.7	275	5	US-10-450-763-37636
5	1153	95.4	230	4	US-10-210-130-56
6	1153	95.4	230	4	US-10-236-417-60
7	1125	93.1	230	3	US-09-988-982-3
8	1056	87.4	208	4	US-10-131-487A-185
9	1038	85.9	219	4	US-10-106-698-5793
10	1028	85.1	208	3	US-09-988-982-1
11	926	76.7	182	4	US-10-236-417-62
12	841	69.6	231	4	US-10-359-499-7
13	807	66.8	230	4	US-10-237-271-17
14	752	62.3	226	5	US-10-868-577A-66
15	752	62.3	226	5	US-10-868-549-25
16	671	55.5	166	4	US-10-237-271-18
17	671	55.5	166	4	US-10-408-765A-2060
18	644	53.3	146	4	US-10-408-765A-2111
19	596	49.3	216	6	US-11-097-143-28815
20	568	47.1	236	3	US-09-934-392-4
21	510.5	42.3	333	4	US-10-369-493-5135
22	438	36.3	297	4	US-10-369-493-3623
23	381	31.5	89	5	US-10-450-763-37635
24	363.5	30.1	222	4	US-10-369-493-8533
25	356	29.5	227	4	US-10-369-493-22321
26	329.5	27.3	220	4	US-10-369-493-9253
27	326.5	27.0	224	4	US-10-369-493-17607

28	326	27.0	213	4	US-10-369-493-19681	Sequence 19681, A
29	323.5	26.8	220	4	US-10-369-493-9472	Sequence 9472, Ap
30	306	25.3	218	4	US-10-369-493-13757	Sequence 13757, A
31	300.5	24.9	215	4	US-10-282-122A-61109	Sequence 61109, A
32	300.5	24.9	502	4	US-10-437-963-150122	Sequence 150122, A
33	299	24.8	265	4	US-10-425-114-48899	Sequence 48899, A
34	296	24.5	235	6	US-11-097-143-14268	Sequence 14268, A
35	294.5	24.4	218	4	US-10-369-493-15372	Sequence 15372, A
36	294	24.3	218	4	US-10-282-122A-68326	Sequence 68326, A
37	290.5	24.0	197	4	US-10-369-493-15739	Sequence 15739, A
38	290.5	24.0	202	4	US-10-369-493-16125	Sequence 16125, A
39	290	24.0	295	4	US-10-369-493-12843	Sequence 12843, A
40	289.5	24.0	221	4	US-10-425-115-367055	Sequence 367055, A
41	286.5	23.7	257	4	US-10-437-963-186726	Sequence 186726, A
42	285.5	23.6	221	4	US-10-767-701-40205	Sequence 40205, A
43	284	23.5	253	4	US-10-424-599-263325	Sequence 263325, A
44	280.5	23.2	258	4	US-10-424-599-145994	Sequence 145994, A
45	277.5	23.0	255	4	US-10-425-115-212412	Sequence 212412, A

ALIGNMENTS

RESULT 1
US-10-236-417-64
; Sequence 64, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 64
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-64

Query Match 99.7%; Score 1204; DB 4; Length 230;
Best Local Similarity 99.6%; Pred. No. 1.5e-119;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MCGNNMSTPLPAIVPAARKATAAIFLHGLDGTGHWAEAFAGIRSHIKYICPHAPVRP	60
Db	1	MCGNNMSTPLPAIVPAARKATAAIFLHGLDGTGHWAEAFAGIRSHIKYICPHAPVRP	60
QY	61	VTLMNVAMPSPWFDIIGLSPDSESGIKQAENIKALIDQVKGIPNSRIILGGFSQ	120
Db	61	VTLMNVAMPSPWFDIIGLSPDSESGIKQAENIKALIDQVKGIPNSRIILGGFSQ	120

QY 181 FGSALTVEKLTLPANVNTFKYEGNMHSSCOQEMDMVKQFIDKLLPPID 230
Db 226 FGSALTVEKLTLPANVNTFKYEGNMHSSCOQEMDMVKQFIDKLLPPID 275

RESULT 5

US-10-210-130-56
; Sequence 56, Application US/10210130
; Publication No. US20040014053A1

GENERAL INFORMATION:

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Fatturajan, Meera

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Miller, Charles E.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Li, Li

; APPLICANT: Berghs, Constance

; APPLICANT: Zhong, Mei

; APPLICANT: Casman, Stacie J.

; APPLICANT: Voss, Edward Z.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Smithson, Glenda

; APPLICANT: Ji, Weizhen

; APPLICANT: Gorman, Linda

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Leite, Mario W.

; APPLICANT: Guo, Xiaojia Sasha

; APPLICANT: Anderson, David W.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: Ort, Tatiana

; APPLICANT: Ellerman, Karen

; APPLICANT: Rastelli, Luca

; APPLICANT: Agee, Michele L.

; APPLICANT: Chaudhuri, Amitabha

; APPLICANT: Chant, John S.

; APPLICANT: DiPippo, Vincent A.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Bisen, Andrew J.

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Giot, Loic

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Spaderna, Steven K.

; APPLICANT: Hjal, Tord

; APPLICANT: Liu, Xiaohong

; APPLICANT: Taupier, Raymond J., Jr.

; APPLICANT: Catterton, Elina

; APPLICANT: Shenoy, Suresh G.

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-416C (Cura-716 SMT)

; CURRENT APPLICATION NUMBER: US/10/210,130

; CURRENT FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: 60/309,501

; PRIOR FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: 60/316,508

; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 60/354,655

; PRIOR FILING DATE: 2002-02-05

; PRIOR APPLICATION NUMBER: 60/310,291

; PRIOR FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: 60/383,887

; PRIOR FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: 60/310,951

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/323,936

; PRIOR FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/381,039

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/323,936

; PRIOR FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/381,039

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/323,936

; PRIOR FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/381,039

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 60/311,292

; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 60/311,979

; PRIOR FILING DATE: 2001-08-13

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 56

; LENGTH: 230

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-210-130-56

Query Match

Best Local Similarity 95.4%; Score 1153; DB 4; Length 230;

Matches 218; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIIPAARKATAAATVFLHGLGDTGHGWAFAFAGIRSSHIIKYICHPAPVRP 60

Db 1 MCGNNMSTPLPTIVPAPRAATTEVFLHGLGDTGHGWAFAFAGIISHHIYICHPAPVRP 60

QY 61 VTLLNNVAMPWFDDIIGLSPDQDESGIKQAANIKALIDQEVKNGIPSNRIILGGFSQ 120

Db 61 VTLLNNVAMPWFDDIIGLSPDQDESGIKQAANIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSLYALTATTOOKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLM 180

Db 121 GGALSLYALTATTOOKLAGVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSALTVEKLTLPANVNTFKYEGNMHSSCOQEMDMVKQFIDKLLPPID 230

Db 181 FGSALTVEKLTLPANVNTFKYEGNMHSSCOQEMDMVKQFIDKLLPPID 230

RESULT 6

US-10-236-417-60

; Sequence 60, Application US/10236417

; Publication No. US20040048256A1

; GENERAL INFORMATION:

; APPLICANT: Agee et al.

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-442C

; CURRENT APPLICATION NUMBER: US/10/236,417

; CURRENT FILING DATE: 2003-01-06

; PRIOR APPLICATION NUMBER: US60/318,120

; PRIOR FILING DATE: 2001-09-01

; PRIOR APPLICATION NUMBER: US60/318,430

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: US60/322,781

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US60/318,184

; PRIOR FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: US60/361,663

; PRIOR FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US60/396,412

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US60/322,636

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US60/322,817

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US60/322,816

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US60/323,519

; PRIOR FILING DATE: 2001-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 341

; SOFTWARE: Custom

; SEQ ID NO 60

; LENGTH: 230

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-236-417-60

Query Match 95.4%; Score 1153; DB 4; Length 230;
Best Local Similarity 94.8%; Pred. No. 4.1e-114;
Matches 218; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSILYLTALTTQOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSILYLTALTTQOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 7
US-09-988-982-3
; Sequence 3, Application US/09988982
; Patent No. US20020081699A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Shah, Purvi
; Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/988,982
; FILING DATE: 19-No. US20020081699A1-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/213,394
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 552244
; LIBRARY: GenBank
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-988-982-3

Query Match 93.1%; Score 1125; DB 3; Length 230;
Best Local Similarity 91.7%; Pred. No. 4e-111;
Matches 211; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSILYLTALTTQOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 121 GGALSILYLTALTTQOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230
DB 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230

RESULT 8
US-10-131-487A-185
; Sequence 185, Application US/10131487A
; Publication No. US20040009478A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TUMOR TISSUE
; FILE REFERENCE: ALBRE 11
; CURRENT APPLICATION NUMBER: US/10/131,487A
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/623,791A
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/DE99/00721
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 185
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-487A-185

Query Match 87.4%; Score 1056; DB 4; Length 208;
Best Local Similarity 90.0%; Pred. No. 7.9e-104;
Matches 207; Conservative 0; Mismatches 1; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAATVFLHGLGDTG-----PVRP 38

QY 61 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 39 VTILNMNVAMPSWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98

QY 121 GGALSILYLTALTTQOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 180
DB 99 GGALSILYLTALTTQOKLAGVTALSCWLPRLASLPQGPPIGGANRDISILOCHGDCDPLVPLM 158

QY 181 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 230
DB 159 FGSLTVEKLTILNPNANVTFTKTEGMMHSSCCQEMMDVKQFIDKLLPPID 208

RESULT 9
US-10-106-698-5793
; Sequence 5793, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid
; FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 5793
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (43)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5793

Query Match 85.9%; Score 1038; DB 4; Length 219;
Best Local Similarity 89.1%; Pred. No. 7e-102; Mismatches 0; Indels 22; Gaps 1;
Matches 205; Conservative 0; Mismatches 0; Indels 22; Gaps 1;
QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 12 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 49
QY 61 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 50 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 109
QY 121 GGALSLYTALTTOOKLAGVTALSCWPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
DB 110 GGALSLYTALTTOOKLAGVTALSCWPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 169
QY 181 FGSLTVEKLKTLVNPANVTFTKTEGMMHSSCQEMMDVKQFIDKLLPPID 230
DB 170 FGSLTVEKLKTLVNPANVTFTKTEGMMHSSCQEMMDVKQFIDKLLPPID 219

RESULT 10
US-09-988-982-1
Sequence 1, Application US/09988982
Patent No. US20020081699A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Shah, Purvi
Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,982
FILING DATE: 19-No. US20020081699A1-2001
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT19
CLONE: 2676650
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-988-982-1

Query Match 85.1%; Score 1028; DB 3; Length 208;
Best Local Similarity 88.7%; Pred. No. 7.6e-101; Mismatches 4; Indels 22; Gaps 1;
Matches 204; Conservative 0; Mismatches 4; Indels 22; Gaps 1;
QY 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 60
DB 1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTGHWAEAFAGIRSHIKYICPHAPVRP 38
QY 61 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 120
DB 39 VTLNMVAMPSWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 98
QY 121 GGALSLYTALTTOOKLAGVTALSCWPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 180
DB 99 GGALSLYTALTTOOKLAGVTALSCWPLRASLPQGPFGIGGANRDISILOCHGDCDPLVPLM 158
QY 181 FGSLTVEKLKTLVNPANVTFTKTEGMMHSSCQEMMDVKQFIDKLLPPID 230
DB 159 FGSLTVEKLKTLVNPANVTFTKTEGMMHSSCQEMMDVKQFIDKLLPPID 208

RESULT 11
US-10-236-417-62
Sequence 62, Application US/10236417
Publication No. US20040048256A1
GENERAL INFORMATION:
APPLICANT: Agee et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442C
CURRENT APPLICATION NUMBER: US/10/236,417
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US60/318,120
PRIOR FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: US60/318,430
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US60/322,781
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US60/318,184
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US60/361,663
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US60/396,412
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US60/322,636
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US60/322,817
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US60/322,816
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US60/323,519
PRIOR FILING DATE: 2001-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 62
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-62

Query Match          76.7%; Score 926; DB 4; Length 182;
Best Local Similarity 78.7%; Pred. No. 4.7e-90;
Matches 181; Conservative 0; Mismatches 1; Indels 48; Gaps 1;

QY 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 VTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFS- 119

QY 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 120 -----QCHGDCDPLVPLM 132

QY 181 FGSLTVEKLTILNPNANVTFTKTYEGMMHSSCOQEMDMVKQFIDKLLPPID 230
Db 133 FGPLTVEKLTILNPNANVTFTKTYEGMMHSSCOQEMDMVKQFIDKLLPPID 182

RESULT 12
US-10-359-499-7
; Sequence 7, Application US/10359499
; Publication No. US20030148363A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; FILE REFERENCE: PF-0470-1 CIP
; CURRENT APPLICATION NUMBER: US/10/359,499
; CURRENT FILING DATE: 2003-02-05
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/013,881
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030148363A1 2768301
US-10-359-499-7

Query Match          69.6%; Score 841; DB 4; Length 231;
Best Local Similarity 67.2%; Pred. No. 7.6e-81;
Matches 156; Conservative 31; Mismatches 41; Indels 4; Gaps 2;

QY 1 MCGNNMSTPL---PAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAP 57
Db 1 MCGNTWSVPLLTDAATVGAERETAIVFLHGLGDTGHGWADALSTIRLPHVKYICPHAP 60

QY 58 VRPVTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGG 117
Db 61 RIPVTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGG 120

QY 118 FSQGGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLV 177
Db 117 -----QCHGDCDPLV 132

; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 62
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-237-271-17

Query Match          66.8%; Score 807; DB 4; Length 230;
Best Local Similarity 72.2%; Pred. No. 3.2e-77;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 XXXXXXXXXXXXXFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTILNPNANVTFTKTYEGMMHSSCOQEMDMVKQFIDKLLPPID 230
Db 181 FGSLTVEKLTILNPNANVTFTKTYEGMMHSSCOQEMDMVKQFIDKLLPPID 230

RESULT 13
US-10-237-271-17
; Sequence 17, Application US/10237271
; Publication No. US20030096328A1
; GENERAL INFORMATION:
; APPLICANT: THE BURNHAM INSTITUTE
; APPLICANT: SMITH, Jeffrey W.
; APPLICANT: KRIDEL, Steven J.
; APPLICANT: AXELROD, Fumiko T.
; TITLE OF INVENTION: SERINE/THREONINE HYDROLASE PROTEINS AND SCREENING ASSAYS
; FILE REFERENCE: BURN100-1
; CURRENT APPLICATION NUMBER: US/10/237,271
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 60/317,842
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (35)..(72)
; OTHER INFORMATION: Xaa is any Amino Acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (96)..(120)
; OTHER INFORMATION: Xaa is any Amino Acid
US-10-237-271-17

Query Match          66.8%; Score 807; DB 4; Length 230;
Best Local Similarity 72.2%; Pred. No. 3.2e-77;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60
Db 1 MCGNNMSTPLPAIIPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKYICPHAPVRP 60

QY 61 VTLMNVAMPWFDFIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
Db 61 XXXXXXXXXXXXXFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120

QY 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180
Db 121 GGALSILYALTATTQOKLAGVTALSCWLPPLRASLPQGPIGGANRDISILOCHGDCDPLVPLM 180

QY 181 FGSLTVEKLTILNPNANVTFTKTYEGMMHSSCOQEMDMVKQFIDKLLPPID 230
Db 181 FGSLTVEKLTILNPNANVTFTKTYEGMMHSSCOQEMDMVKQFIDKLLPPID 230

RESULT 14
US-10-868-577A-66
; Sequence 66, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
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Job time : 169 secs

; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-868-577A-66

Query Match 62.3%; Score 752; DB 5; Length 226;
Best Local Similarity 63.9%; Pred. No. 2.3e-71;
Matches 145; Conservative 27; Mismatches 51; Indels 4; Gaps 2;
QY 6 MSTPL---PAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKICHPAPVRPVT 62
DB 1 MSVPLLTDAATVSGARETAIAVFLHGLGDTGHGWAFAFAGIRSSHIIKICHPAPVRPVT 60
QY 63 LNNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGG 122
DB 61 LNNKMWPSWFDLWGLSPDAPDEAGIKKAENIKALIEHEMKNKGIIPANRIVLGGFSQGG 120
QY 123 ALSLYTALTTOOKLAGVTALSCWLPRLASLPQGPFGANRDISILOCHGDCDPLVPLMFG 182
DB 121 ALSLYTALTCPHLAGIVALSCWLPRLHRAFPQAANGSA-RTWPYSSAMGSWTLPVRF 179
QY 183 SLTVEKLTIVNPANTVFTKTYEGMHSSCOQEMMDVKQFIDKLLPPI 229
DB 180 ALTAELKRSVVTARVQFKTPGVHSSCPQEMAAVKEFLEKLLPPV 226

RESULT 15
US-10-868-549-25
; Sequence 25, Application US/10868549
; Publication No. US20050043235A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
; FILE REFERENCE: 28967/39117A
; CURRENT APPLICATION NUMBER: US/10/868,549
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,114
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-868-549-25

Query Match 62.3%; Score 752; DB 5; Length 226;
Best Local Similarity 63.9%; Pred. No. 2.3e-71;
Matches 145; Conservative 27; Mismatches 51; Indels 4; Gaps 2;
QY 6 MSTPL---PAIVPAARKATAAIVFLHGLGDTGHGWAFAFAGIRSSHIIKICHPAPVRPVT 62
DB 1 MSVPLLTDAATVSGARETAIAVFLHGLGDTGHGWAFAFAGIRSSHIIKICHPAPVRPVT 60
QY 63 LNNVAMPSPWFDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGG 122
DB 61 LNNKMWPSWFDLWGLSPDAPDEAGIKKAENIKALIEHEMKNKGIIPANRIVLGGFSQGG 120
QY 123 ALSLYTALTTOOKLAGVTALSCWLPRLASLPQGPFGANRDISILOCHGDCDPLVPLMFG 182
DB 121 ALSLYTALTCPHLAGIVALSCWLPRLHRAFPQAANGSA-RTWPYSSAMGSWTLPVRF 179
QY 183 SLTVEKLTIVNPANTVFTKTYEGMHSSCOQEMMDVKQFIDKLLPPI 229
DB 180 ALTAELKRSVVTARVQFKTPGVHSSCPQEMAAVKEFLEKLLPPV 226

Search completed: April 13, 2006, 21:33:11

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OM protein - protein search, using sw model

Run on: April 13, 2006, 21:30:37 ; Search time 27 Seconds
(without alignments)
361.945 Million cell updates/sec

Title: US-09-493-601B-2
Perfect score: 1208
Sequence: 1 MCGNNMSTPLPAIVPARKA.....CQEMMDVKQFDKLLPPID 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA New.*
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 - 2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	199	16.5	169	5	US-09-978-360A-443
2	92	7.6	141	7	US-11-084-508-22
3	87	7.2	338	7	US-11-096-568A-29329
4	87	7.2	346	7	US-11-096-568A-29328
5	87	7.2	353	7	US-11-096-568A-29327
6	87	7.2	397	7	US-11-084-508-5
7	85.5	7.1	373	7	US-11-087-099-4020
8	83.5	6.9	223	7	US-11-096-568A-30586
9	83.5	6.9	279	7	US-11-096-568A-30585
10	83.5	6.9	318	7	US-11-096-568A-30584
11	83	6.9	379	7	US-11-098-686-10741
12	83	6.9	666	7	US-11-072-512-3618
13	82	6.8	616	6	US-10-131-826A-206
14	82	6.8	616	6	US-10-973-115B-206
15	82	6.8	616	6	US-11-290-153-206
16	81	6.7	129	7	US-11-096-568A-12706
17	81	6.7	462	7	US-11-087-099-2138
18	80.5	6.7	462	7	US-11-087-099-5753
19	80.5	6.7	484	7	US-11-188-298-6763
20	80	6.6	299	6	US-10-454-437-228
21	78.5	6.5	631	7	US-11-188-298-3431
22	77.5	6.4	637	7	US-11-079-463-6936
23	77	6.4	256	7	US-11-179-977-2
24	77	6.4	415	7	US-11-079-463-9641
25	77	6.4	481	7	US-11-188-298-3813

26	76.5	6.3	286	7	US-11-079-463-7162	Sequence 7162, Ap
27	76.5	6.3	339	6	US-10-995-076-2	Sequence 2, Appli
28	76.5	6.3	359	7	US-11-098-686-10361	Sequence 10361, A
29	76	6.3	401	7	US-11-096-568A-29666	Sequence 29666, A
30	76	6.3	402	7	US-11-096-568A-29665	Sequence 29665, A
31	76	6.3	520	7	US-11-096-568A-29664	Sequence 29664, A
32	75.5	6.2	269	6	US-10-495-597-14	Sequence 14, Appl
33	75.5	6.2	291	7	US-11-020-602-227	Sequence 227, App
34	75.5	6.2	339	6	US-10-995-076-1	Sequence 1, Appli
35	75.5	6.2	366	7	US-11-087-099-6135	Sequence 6135, Ap
36	75.5	6.2	1972	7	US-11-124-367A-446	Sequence 446, App
37	75	6.2	332	7	US-11-096-568A-19004	Sequence 19004, A
38	75	6.2	441	6	US-10-995-561-638	Sequence 638, App
39	75	6.2	441	6	US-10-995-561-639	Sequence 639, App
40	75	6.2	441	7	US-11-108-519-14	Sequence 14, Appl
41	75	6.2	441	7	US-11-141-554B-14	Sequence 14, Appl
42	74.5	6.2	256	7	US-11-096-568A-20324	Sequence 20324, A
43	74.5	6.2	271	7	US-11-096-568A-20323	Sequence 20323, A
44	74.5	6.2	296	7	US-11-096-568A-20322	Sequence 20322, A
45	74.5	6.2	315	7	US-11-096-568A-12749	Sequence 12749, A

ALIGNMENTS

RESULT 1
US-09-978-360A-443
; Sequence 443, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 443
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -88..-1
US-09-978-360A-443

Query Match 16.5%; Score 199; DB 5; Length 169;
Best Local Similarity 33.8%; Pred. No. 1.6e-12;


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; LENGTH: 353
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(353)
; OTHER INFORMATION: Ceres Seq. ID no. 4811687
US-11-096-568A-29327

Query Match
Best Local Similarity 7.2%; Score 87; DB 7; Length 353;
Matches 34; Conservative 20; Mismatches 62; Indels 30; Gaps 6;

QY 19 KATAVIFLHGLGDTGCHGWAEEAFAGIRSSHIIKICHPAPVREVTLMNNAVPSWFDIIGL 78
Db 24 KEGPVLLHGFDPDLWYWRHQISGLSSLYRAVAP-----DLRGY 64

QY 79 SPDSQDESGIKQAENI-----KALIDQEVKNGIPSNRIILGFSQGGALSALTATLTTQQ 134
Db 65 G-DSDSPESFSEYTCINVVGDVLALLDSVAGN---QEKVFLVGHWDGAIIGWFLCLFRPE 120

QY 135 KLAGVTALSCWLPRLASLPQ-CPIGG 159
Db 121 KINGFVCLS--VPYRSRNPVKRPEVQG 144

RESULT 6
US-11-084-508-5
; Sequence 5, Application US/11084508
; Publication No. US20050260737A1
; GENERAL INFORMATION:
; APPLICANT: Rahman, Raja Noor Zaliha Abd.
; APPLICANT: Salleh, Abu Bakar
; APPLICANT: Basri, Mahiran
; TITLE OF INVENTION: Novel Lipase Gene from Bacillus sphaericus 205y
; FILE REFERENCE: KAN-101
; CURRENT APPLICATION NUMBER: US/11/084,508
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: MY 20040958
; PRIOR FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Bacillus sphaericus
US-11-084-508-5

Query Match
Best Local Similarity 7.2%; Score 87; DB 7; Length 397;
Matches 63; Conservative 28; Mismatches 82; Indels 108; Gaps 14;

QY 15 PAARKA---TAAVIFLHG---LGDTG--HGWAEEAF--AGIRSSHIIKICHPAPVRYT 62
Db 151 PAKKSEDLVTPVIVQVHGGWVGDKQVQDWNQWMDQGYTFVDQYRMP-----PVA 205

QY 63 LMNVAMPWFPIIGLSPDQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQGG 122
Db 206 -----GWKDEVG--DVKSAIGWIVQHADTYK-----IDPNRIILMGESAGG 244

QY 123 ALSLYTALTQQKLAGVTALSCWLPRLASLPQ----- 156
Db 245 NLAMLAAYSLGDK-----HLPSTDPDVPDIKAVINMYGPSDMTAFYKNNPSKRVY 295

QY 157 -----IGANRD-----ISILQCH-----GDCDPLVPLMFGSLTVKELKT 191
Db 296 QVLDQYIGSPSDYPARVKULSPIYIEHPPTIMFLGTGDIRIVPVEQANVLDKLT 355

QY 192 -----LVNPNANVFTKTEGMMHSSCCQEMMDVKQFIDK 224
Db 356 SGVAHELXLLPKVDHGHGFANDPGSLSTQFAKE--KVKAFLQK 394
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RESULT 7
US-11-087-099-4020
; Sequence 4020, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4020
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Methanocaldococcus jannaschii
US-11-087-099-4020

Query Match
Best Local Similarity 7.1%; Score 85.5; DB 7; Length 373;
Matches 40; Conservative 39; Mismatches 60; Indels 55; Gaps 9;

QY 51 YICHPAPVRPVTLMNNAVPSWFDIIGLSPDQDESGIKQAEN-----IKALIDQEV 104
Db 57 YVINKADLVPKDI-----LEKKEVFG-----ENTVFSAKRRLGTLKILREMIKQSL 103

QY 105 KN-GIPSNRIILGFSQGGALSALTATLTTQK-----LAGVTALSCWLPRLASLPQGP 158
Db 104 KEMGKKEGVGIVGYPNVGKSSIIINALTKRKALTGSAVLTKGEQWVRL----- 153

QY 159 GANRDISILQCHG-----DCDPLVPLMFGSLTVKELTLVNPA-----NVTFTK 202
Db 154 --TKNIKLMDTGPVLEMRDEDLV--ISGALREKVENIPPALKILSRINNFDNSIIKE 209

QY 203 YEGMMHSSCCQEMM 216
Db 210 YFGVDYEEVDELL 223

RESULT 8
US-11-096-568A-30586
; Sequence 30586, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30586
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(223)
; OTHER INFORMATION: Ceres Seq. ID no. 4963864
US-11-096-568A-30586

Query Match
Best Local Similarity 6.9%; Score 83.5; DB 7; Length 223;
Matches 51; Conservative 22; Mismatches 86; Indels 75; Gaps 8;

QY 30 LGDTG-----HGWAEEAFAGIRSSHIIKICHPAPVRPVTLMNNAVPSWFDIIGLS 83
Db 29 IGITIGLSGMEHAFAAADTRYVVVPLIGVQLNKIAATMRPILPCM-----SEY 80

QY 84 EDESGIKQAENI-----KALIDQEVKNGIPSNRIILGFSQGG 122
Db 81 EDGFGFRWAINDWEARVNSIKPLFEARIDLGKNIIDKELVEKY-WNRIAPG----- 133
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QY 123 ALSLYTALTTOQKLAGVTALSCWLPRLASLPQGPICGANRDISILQCHGDCDPLVPLMFG 182
Db 134 -----LASKFSPYSPLPVIAPRPLYILNGAN-----DPRCPL--G 166

QY 183 SLTV-----EKLKTLVNPANVTFTYEGMHSSCOQEMDMVKQFIDKLLPPID 230
Db 167 GLELALKRAEKAYKETASPGNFKFAEDGVGHEATSFMIKESDWDKFLKQED 220

RESULT 9
US-11-096-568A-30585
; Sequence 30585, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30585
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(279)
; OTHER INFORMATION: Ceres Seq. ID no. 4963863
US-11-096-568A-30585

Query Match 6.9%; Score 83.5; DB 7; Length 279;
Best Local Similarity 21.8%; Pred. No. 1.2; Mismatches 86; Indels 75; Gaps 8;
Matches 51; Conservative 22;

QY 30 LGDTG-----HGWAFAFAGIRSSHIKYICPHAPVRPVTLMNVMAMPWFDIIGLSPDSQ 83
Db 85 IGTIGTSLGGMAWFAAAADTRYVVVPLIGVQLNKIAATMRPILPCM-----SEY 136

QY 84 EDESGIKQAAENI-----KALIDQEVKNGIPSNRIILGGFSQGG 122
Db 137 EDGFGFRWAIDENEWEARNVSIKPLFEARIDLGKNIIDKELVEKV-WNRIAPG----- 189

QY 123 ALSLYTALTTOQKLAGVTALSCWLPRLASLPQGPICGANRDISILQCHGDCDPLVPLMFG 182
Db 190 -----LASKFSPYSPLPVIAPRPLYILNGAN-----DPRCPL--G 222

QY 183 SLTV-----EKLKTLVNPANVTFTYEGMHSSCOQEMDMVKQFIDKLLPPID 230
Db 223 GLELALKRAEKAYKETASPGNFKFAEDGVGHEATSFMIKESDWDKFLKQED 276

RESULT 10
US-11-096-568A-30584
; Sequence 30584, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30584
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(318)
; OTHER INFORMATION: Ceres Seq. ID no. 4963862
US-11-096-568A-30584
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Query Match 6.9%; Score 83.5; DB 7; Length 318;
Best Local Similarity 21.8%; Pred. No. 1.5; Mismatches 86; Indels 75; Gaps 8;
Matches 51; Conservative 22;

QY 30 LGDTG-----HGWAFAFAGIRSSHIKYICPHAPVRPVTLMNVMAMPWFDIIGLSPDSQ 83
Db 124 IGTIGTSLGGMAWFAAAADTRYVVVPLIGVQLNKIAATMRPILPCM-----SEY 175

QY 84 EDESGIKQAAENI-----KALIDQEVKNGIPSNRIILGGFSQGG 122
Db 176 EDGFGFRWAIDENEWEARNVSIKPLFEARIDLGKNIIDKELVEKV-WNRIAPG----- 228

QY 123 ALSLYTALTTOQKLAGVTALSCWLPRLASLPQGPICGANRDISILQCHGDCDPLVPLMFG 182
Db 229 -----LASKFSPYSPLPVIAPRPLYILNGAN-----DPRCPL--G 261

QY 183 SLTV-----EKLKTLVNPANVTFTYEGMHSSCOQEMDMVKQFIDKLLPPID 230
Db 262 GLELALKRAEKAYKETASPGNFKFAEDGVGHEATSFMIKESDWDKFLKQED 315

RESULT 11
US-11-098-686-10741
; Sequence 10741, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kaput, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/416,395
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10741
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10741

Query Match 6.9%; Score 83; DB 7; Length 379;
Best Local Similarity 26.8%; Pred. No. 2.1; Mismatches 53; Indels 28; Gaps 6;
Matches 37; Conservative 20;

QY 12 AIVPA-ARKATAAVIFPLHGLGDTGHGWAFAFAGIRSSHIKYICPHAPVRPVTLMNVMAMP 70
Db 19 AIIPSHASEPIKIGVYPLTGTQNAVGGQLELDGKLAH-----DLNPVVLNRPVQL- 69

QY 71 SWFDIIGLSPDSQDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTAL 130
Db 70 -----FIVDNKSDK---VEAANAVKRLIDQD-----KVCVIIG--SYGSSLSLAGGE 111

QY 131 TTQOKLAGVTALSCWLP 148
Db 112 VAEQAKIPVIGTCTNPL 129

RESULT 12
US-11-072-512-3618
; Sequence 3618, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
```

```

; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3618
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-3618

Query Match      6.9%; Score 83; DB 7; Length 666;
Best Local Similarity 18.4%; Pred. No. 4.5; Mismatches 104; Indels 88; Gaps 8;
Matches 51; Conservative 34;

QY 16 AARKATAAIVFL-----HGLGDTGHGWAFAF-----AGIRSSH-----IKYIC 53
Db 89 ACKRAAKSLIKLGLERFHGVGILGFNSAEWFTAVGAILAGLCVGIYATNSAEVCQYI 148
QY 54 -----PHAPVRPVTLMNVAMP-----SWFDIIGLS---P 80
Db 149 THAKVNILLVENDQQLKILSIPOSSLEPLKAIQVRLPMKNNLYSWDDFMELGRSIP 208
QY 81 DSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTALTQOKLA--- 137
Db 209 DTQLEQVIESOKANQCAVLIYTSGTGTPKGWML-----SHDNITWIAGAVTKDFKLTDXH 264
QY 138 -----GVTALSCWLPURASLPQGPPIGGANRDISILOCHGDCDPLVPLMFGSLT 185
Db 265 ETVSVYLPISHIAAQMMDIWVPIK-----IGALTYFAQADALKGTLVSTLK 310
QY 186 VEKLKTLVNPANVTFTKTYEGMHSSCQOEMMDVKQFI 222
Db 311 EVKPTVFIGVPIQWEKIHVMVKNSAKSMGLKKKAFV 347

RESULT 13
US-10-131-826A-206
; Sequence 206, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 206
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-131-826A-206

Query Match      6.8%; Score 82; DB 6; Length 616;
Best Local Similarity 19.4%; Pred. No. 5.1;
Matches 54; Conservative 32; Mismatches 101; Indels 92; Gaps 9;

QY 16 AARKATAAIVFL-----HGLGDTGHGWAFAF-----AGIRSSH-----IKYIC 53
Db 39 ACKRAAKSLIKLGLERFHGVGILGFNSAEWFTAVGAILAGLCVGIYATNSAEVCQYI 98
QY 54 PHAPVR-----PVTLMNVAMPSPFDIIGLS--- 79
Db 99 THAKVNILLVENDQQLKILSIPOSSLEPLKAIQVRLPMKNNN--LYSWDDFMELGRS 156
QY 80 -PDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTALTQOKLA- 137
Db 157 IPTQLEQVIESOKANQCAVLIYTSGTGTPKGWML-----SHDNITWIAGAVTKDFKLT 212
QY 138 -----GVTALSCWLPURASLPQGPPIGGANRDISILOCHGDCDPLVPLMFGS 183
Db 213 KHETVVSVYLPISHIAAQMMDIWVPIK-----IGALTYFAQADALKGTLVST 258
QY 184 LTVEKLKTLVNPANVTFTKTYEGMHSSCQOEMMDVKQFI 222
Db 259 LKEVKPTVFIGVPIQWEKIHVMVKNSAKSMGLKKKAFV 297

RESULT 14
US-10-973-115B-206
; Sequence 206, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
```

```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 206
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-973-115B-206

Query Match 6.8%; Score 82; DB 6; Length 616;
Best Local Similarity 19.4%; Pred. No. 5.1;
Matches 54; Conservative 32; Mismatches 101; Indels 92; Gaps 9;

QY 16 AARKATAAVIFL-----HGLGDTGHGWAFAF-----AGIRSSH-----IKYIC 53
Db 39 ACRKAASLIKGLERFHGVGILGFNSAEWFITAVGAILAGGLCVGIYATNSAEACQYVI 98
QY 54 PHAPVR-----PVTLMNVAMPSPWFDIIGLS-- 79
Db 99 THAKVNILVENDQLOKILSIPOSSLEPLKALIQVRLPMKNN--LYSWDDFMELGRS 156
QY 80 -PDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSXYALTTOOKLA- 137
Db 157 IPTQLEQVIESQKANCQCAVLIYTSGTGIPKGVM-----SHDNITWIAGAVTKDFKLT 212
QY 138 -----GVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLMFGS 183
Db 213 KHETVVSYPPLSHIAAQMMDIWVPIK-----IGALTTFQAQADALKGTLVST 258
QY 184 LTVEKLTVLNPNANTVTKTYEGMHSSCOQEMDMVKOFI 222
Db 259 LKEVKPTVFIGVPIQWEKIHEMWKNSAKSMGLKKKAFV 297

RESULT 15
US-11-290-153-206
; Sequence 206, Application US/11290153
; Publication No. US20060073568A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C321
; CURRENT APPLICATION NUMBER: US/11/290,153
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: US/10/146,728
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 206
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-11-290-153-206

Query Match 6.8%; Score 82; DB 7; Length 616;
Best Local Similarity 19.4%; Pred. No. 5.1;
Matches 54; Conservative 32; Mismatches 101; Indels 92; Gaps 9;

QY 16 AARKATAAVIFL-----HGLGDTGHGWAFAF-----AGIRSSH-----IKYIC 53
Db 39 ACRKAASLIKGLERFHGVGILGFNSAEWFITAVGAILAGGLCVGIYATNSAEACQYVI 98
QY 54 PHAPVR-----PVTLMNVAMPSPWFDIIGLS-- 79
Db 99 THAKVNILVENDQLOKILSIPOSSLEPLKALIQVRLPMKNN--LYSWDDFMELGRS 156
QY 80 -PDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGGALSXYALTTOOKLA- 137
Db 157 IPTQLEQVIESQKANCQCAVLIYTSGTGIPKGVM-----SHDNITWIAGAVTKDFKLT 212
QY 138 -----GVTALSCWLPRLASLPQGPIGGANRDISILOCHGDCDPLVPLMFGS 183
Db 213 KHETVVSYPPLSHIAAQMMDIWVPIK-----IGALTTFQAQADALKGTLVST 258
QY 184 LTVEKLTVLNPNANTVTKTYEGMHSSCOQEMDMVKOFI 222
Db 259 LKEVKPTVFIGVPIQWEKIHEMWKNSAKSMGLKKKAFV 297

Search completed: April 13, 2006, 21:33:44
Job time : 29 secs
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